

GenCore version 5.1.7
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OM protein - protein search, using SW model

Run on: February 16, 2006, 16:57:42 / Search time 186 Seconds
(without alignments)
944.901 Million cell updates/sec

Title: US-10-618-570-2
Perfect score: 2059
Sequence: 1 MAQMDPDPDQEDTDSCTES.....DKATRVGINIFTRLTKQE 400

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 2443163 seqs, 439378781 residues
Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: A_GeneSeq_21:*

1:	geneSeqp19808:*
2:	geneSeqp19908:*
3:	geneSeqp20008:*
4:	geneSeqp20018:*
5:	geneSeqp20028:*
6:	geneSeqp20038:*
7:	geneSeqp20038:*
8:	geneSeqp20048:*
9:	geneSeqp20058:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2059	100.0	400	2	AAV03098 Bovine sc
2	1381	67.1	349	2	AAV05508 Scavenger
3	1381	67.1	453	2	AAV05509 Scavenger
4	1381	67.1	453	2	AAV07036 Bovine so
5	1047.5	50.9	451	2	AAV19708 Macrophag
6	1046.5	50.8	451	2	AD162129 Human sca
7	1042.5	50.6	358	2	AAV21513 Human sca
8	1042.5	50.6	358	2	AAV40803 Human sca
9	1042.5	50.6	358	2	AAV08078 Type II m
10	1042.5	50.6	358	4	AAV49716 Human typ
11	1042.5	50.6	358	7	ADB89003 Human mac
12	1042.5	50.6	358	8	ADQ39735 Human myo
13	1042.5	50.6	358	8	ADQ39731 Human myo
14	1042.5	50.6	358	8	ADQ39734 Human myo
15	1042.5	50.6	358	8	ADQ39733 Human myo
16	1042.5	50.6	451	2	AAV21512 Human sca
17	1042.5	50.6	451	2	AAV40802 Human sca
18	1042.5	50.6	451	3	AAV08077 Type I ma
19	1042.5	50.6	451	3	AAV000080 Protein o
20	1042.5	50.6	451	4	AAV49715 Human typ
21	1042.5	50.6	451	8	AD162127 Human mac
22	1042.5	50.6	451	8	AD162123 Human mac
23	1042.5	50.6	451	8	AD162125 Human mac
24	1042.5	50.6	451	8	AD162126 Human mac

25	1042.5	50.6	451	8	AD162124 Human mac
26	1042.5	50.6	451	8	AD114197 Novel hum
27	1042.5	50.6	451	8	ADQ39732 Human myo
28	1042.5	50.6	451	8	ADP45547 Homologue
29	1042.5	50.6	487	8	ADP24729 PRO Polyp
30	1040.5	50.5	451	8	AD162128 Human mac
31	1039.5	50.5	451	8	AD162130 Human mac
32	1034.5	50.2	451	8	AD162131 Human mac
33	1032.5	50.1	451	8	AAV27035 Human sol
34	801	38.9	454	7	ADP28571 Murine ma
35	801	38.9	458	8	ADP45554 Mouse typ
36	680.5	33.1	502	8	ADP97493 Circular-IgC
37	678.5	33.0	581	9	AAV28082 Circular-IgC
38	678	32.9	128	9	ADV78149 Chicken I
39	678	32.9	152	2	AAV29307 Wild-type
40	678	32.9	152	2	AAV17867 Chicken a
41	678	32.9	152	8	ADP26980 Chicken a
42	678	32.9	152	8	AAV28059 Chicken a
43	678	32.9	153	9	ADV78159 Barley am
44	678	32.9	161	3	AAV44699 Potato pr
45	678	32.9	269	8	ADP97489 CD1d-IgG-

ALIGNMENTS

RESULT 1
AAV03098
ID AAV03098 standard; protein, 400 AA.

AC AAV03098;
XX
XX
DT 03-DEC-1999 (first entry)
XX
DE Bovine scavenger receptor class A (SCR)/avidin fusion protein.
XX
XX Scavenger receptor class A; SCR; avidin; fusion protein; bovine; ECD;
KW membrane-spanning domain; extracellular domain; biotin-binding activity;
KM endocytosis.
XX
XX Synthetic.
OS Bos taurus.
XX
XX WO9942577-A2.
XX
XX 26-AUG-1999.
XX
XX 23-FEB-1999; 99WO-GB000546.
XX
XX 23-FEB-1998; 98GB-00003757.
PR 24-JUN-1998; 98GB-00013653.
XX
XX (EURO-) EUROGENE LTD.
XX
XX Y1a-Hextuula S, Kulomaa M, Lehtolainen P, Marjomaki V, Airenne K;
DR MPI: 1999-561345/47.
DR N-PSDB; AA029997.
XX
XX New fusion proteins having an extracellular domain with biotin-binding
PT activity, used to target biotinylated molecules to specific sites in
XX tissues.
XX
XX Claim 5; Page 21-23; 23pp; English.
XX
XX This invention describes a novel protein (A) which comprises a membrane-
XX spanning domain and an extracellular domain (ECD), where the ECD
XX comprises biotin-binding activity. Using the proteins or encoding nucleic
XX acid molecules it is possible to target biotinylated molecules to
XX specific sites in tissues. Molecules targeted in this way may be taken up
XX by the tissues or cells by endocytosis, allowing the molecules to exert
XX their effects within or on the cell. This sequence represents a bovine
XX scavenger receptor class A/avidin fusion protein which is used in the

CC description of the invention
XX
SQ Sequence 400 AA;
Query Match 100.0%; Score 2059; DB 2; Length 400;
Best Local Similarity 100.0%; Pred. No. 1.2e-156;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAQMDPDDQEDBDTSCTESYKFPDARSVTALLPPHPKNGPFLQEMKSYKTALLITLYLIV 60
DB 1 MAQMDPDDQEDBDTSCTESYKFPDARSVTALLPPHPKNGPFLQEMKSYKTALLITLYLIV 60
QY 61 FVLVPIIIGIYVAAQLKMETKNCCTVGSVNADISPSPEKGNGSEDEMFREAVMERMSNM 120
DB 61 FVLVPIIIGIYVAAQLKMETKNCCTVGSVNADISPSPEKGNGSEDEMFREAVMERMSNM 120
QY 121 ESRIOYLSDBNEANLLDAKNFQNFSTTTDQRFNDVLFQNSILSSIOEHENIIGDISKSLV 180
DB 121 ESRIOYLSDBNEANLLDAKNFQNFSTTTDQRFNDVLFQNSILSSIOEHENIIGDISKSLV 180
QY 181 GLNTTVLDLPFSITLNGRVOENAFKQOEEMRKLEERYNNAEIKSLDEKQVYLEQIK 240
DB 181 GLNTTVLDLPFSITLNGRVOENAFKQOEEMRKLEERYNNAEIKSLDEKQVYLEQIK 240
QY 241 GEMKLNNITNDLRKWEHSQTLKNITLLQGARCSLTGKWTNDLGSNMTIGAVNSRGE 300
DB 241 GEMKLNNITNDLRKWEHSQTLKNITLLQGARCSLTGKWTNDLGSNMTIGAVNSRGE 300
QY 301 FTGYITLVATSNIEIKSPPLHGTONTINKRQPTFGFTVAMKSEESTTTVFGQCFIDRN 360
DB 301 FTGYITLVATSNIEIKSPPLHGTONTINKRQPTFGFTVAMKSEESTTTVFGQCFIDRN 360
QY 361 GKEVLKTMMLRSSVNDIGDWMKATRVGINIFTRLRTOKE 400
DB 361 GKEVLKTMMLRSSVNDIGDWMKATRVGINIFTRLRTOKE 400
RESULT 2
AAR05508
ID AAR05508 standard; protein; 349 AA.
XX
AC AAR05508;
XX
DT 25-MAR-2003 (revised)
DT 31-OCT-2002 (revised)
DT 23-OCT-1990 (first entry)
XX
DE Scavenger receptor protein with affinity for acylated low density
lipoprotein (aLDL).
XX
KW Acylated low density lipoprotein; aLDL; atherosclerotic plaque; ds.
XX
OS Synthetic.
XX
PN WO9005748-A.
XX
PD 31-MAY-1990.
XX
PE 15-NOV-1988; 88US-00272002.
XX
PR 15-NOV-1988; 88US-00272002.
PR 09-AUG-1989; 89US-00391486.
AX
PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
XX
PI Kodama T, Krieger M;
XX
DR WPI; 1990-193408/25.
DR N-PSDB; AAQ04925.
XX
PT New receptor protein - has affinity for acetylated low density
lipoprotein and corresponding antibodies and DNA sequences.
XX

PS Disclosure; Page ?; 79pp; English.
XX
CC Receptor protein, and fragments and analogues thereof may be immobilised
CC on a support and used in assay and purification of the aLDL target.
CC Labelled Abs, raised to the protein may be injected into the vascular
CC system to detect the presence of atherosclerotic plaques. (Updated on 31-
CC OCT-2002 to add missing OS field.) (Updated on 25-MAR-2003 to correct PR
CC field.) (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-
CC 2003 to correct PI field.)
XX
SQ Sequence 349 AA;
Query Match 67.1%; Score 1381; DB 2; Length 349;
Best Local Similarity 100.0%; Pred. No. 3e-102;
Matches 272; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAQMDPDDQEDBDTSCTESYKFPDARSVTALLPPHPKNGPFLQEMKSYKTALLITLYLIV 60
DB 1 MAQMDPDDQEDBDTSCTESYKFPDARSVTALLPPHPKNGPFLQEMKSYKTALLITLYLIV 60
QY 61 FVLVPIIIGIYVAAQLKMETKNCCTVGSVNADISPSPEKGNGSEDEMFREAVMERMSNM 120
DB 61 FVLVPIIIGIYVAAQLKMETKNCCTVGSVNADISPSPEKGNGSEDEMFREAVMERMSNM 120
QY 121 ESRIOYLSDBNEANLLDAKNFQNFSTTTDQRFNDVLFQNSILSSIOEHENIIGDISKSLV 180
DB 121 ESRIOYLSDBNEANLLDAKNFQNFSTTTDQRFNDVLFQNSILSSIOEHENIIGDISKSLV 180
QY 181 GLNTTVLDLPFSITLNGRVOENAFKQOEEMRKLEERYNNAEIKSLDEKQVYLEQIK 240
DB 181 GLNTTVLDLPFSITLNGRVOENAFKQOEEMRKLEERYNNAEIKSLDEKQVYLEQIK 240
QY 241 GEMKLNNITNDLRKWEHSQTLKNITLLQ 272
DB 241 GEMKLNNITNDLRKWEHSQTLKNITLLQ 272
RESULT 3
AAR05509
ID AAR05509 standard; protein; 453 AA.
XX
AC AAR05509;
XX
DT 25-MAR-2003 (revised)
DT 31-OCT-2002 (revised)
DT 23-OCT-1990 (first entry)
XX
DE Scavenger receptor protein with affinity for acylated low density
lipoprotein (aLDL).
XX
KW Acylated low density lipoprotein; aLDL; atherosclerotic plaque; ds.
XX
OS Synthetic.
XX
PN WO9005748-A.
XX
PD 31-MAY-1990.
XX
PE 15-NOV-1988; 88US-00272002.
XX
PR 15-NOV-1988; 88US-00272002.
PR 09-AUG-1989; 89US-00391486.
AX
PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
XX
PI Kodama T, Krieger M;
XX
DR WPI; 1990-193408/25.
DR N-PSDB; AAQ04925.
XX
PT New receptor protein - has affinity for acetylated low density
lipoprotein and corresponding antibodies and DNA sequences.
XX

PS Disclosure; Page 7; 79pp; English.

XX Receptor protein, and fragments and analogues thereof may be immobilised
CC on a support and used in assay and purification of the aLDL target.
CC Labelled Abs, raised to the protein may be injected into the vascular
CC system to detect the presence of atherosclerotic plaques. (Updated on 31-
CC OCT-2002 to add missing OS field.) (Updated on 25-MAR-2003 to correct PR
CC field.) (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-
CC 2003 to correct PI field.)

XX Sequence 453 AA;

Query Match 67.1%; Score 1381; DB 2; Length 453;

Best Local Similarity 100.0%; Pred. No. 4.3e-102; Mismatches 0; Gaps 0;

Matches 272; Conservative 0; Indels 0; Gaps 0;

QY 1 MAQWDPDPQOEDTDSCTESVFKDARSVTALIPHPKNGPTLQERMKSYKTLITLYLIV 60
DB 1 MAQWDPDPQOEDTDSCTESVFKDARSVTALIPHPKNGPTLQERMKSYKTLITLYLIV 60
QY 61 FVTVLPITIGIYAAQLKMKETKCTGVSNADISPEBKGKNGSEDEMRPREAVMERMSNM 120
DB 61 FVTVLPITIGIYAAQLKMKETKCTGVSNADISPEBKGKNGSEDEMRPREAVMERMSNM 120
QY 121 ESRIOYLSDNENANLDAKNFQNSITTDORFNDVLFOLNSLLSIOEHENITGDISKSLIV 180
DB 121 ESRIOYLSDNENANLDAKNFQNSITTDORFNDVLFOLNSLLSIOEHENITGDISKSLIV 180
QY 181 GIANTTVLDLQFSIETLNGRVQENAFKQOEEMKLEERLYNASAEIKSLDEKQVYLEOEIK 240
DB 181 GIANTTVLDLQFSIETLNGRVQENAFKQOEEMKLEERLYNASAEIKSLDEKQVYLEOEIK 240
QY 241 GEMKLNITNDRLKDMHESQTLKNITLLQG 272
DB 241 GEMKLNITNDRLKDMHESQTLKNITLLQG 272

RESULT 4

ID AAR27036 standard; protein; 453 AA.

AC AAR27036;

DT 23-SEP-2004 (revised)

DT 25-MAR-2003 (revised)

DT 20-MAY-1998 (first entry)

DE Bovine sol. scavenger receptor.

KM Macrophage; endotoxaemia; radiolabelled; toxic; degenerate.

OS Bos taurus.

XX Unidentified.

PH Key Location/Qualifiers
FT Domain 1..50 "cytoplasmic"
FT Domain 51..76
FT Domain /note= "transmembrane"
FT Domain 77..109
FT Domain /note= "spacer"
FT Domain 110..271
FT Domain /note= "alpha helical coiled coil"
FT Domain 272..343
FT Domain /note= "collagen binding"
FT Domain 341..451
FT Domain /note= "Cys-rich"

XX W09214482-A1.

XX 03-SEP-1992.

XX 21-FEB-1992; 92WO-US001370.

XX 22-FEB-1991; 91US-00662227.

XX (MASI) MASSACHUSETTS INST TECHNOLOGY.

XX Krieger M;

XX WPI; 1992-315935/38.

XX N-PSDB; AAQ28540.

PT Treatment and diagnosis of endotoxaemia and related disease states -
PT using a polypeptide fragment of the extracellular portion of a macrophage
PT scavenger receptor protein.

PS Disclosure; Page 38; 56pp; English.

XX The bovine scavenger receptor protein sequence was deduced from the DNA
CC sequence obt'd. by screening a bovine lung cDNA library with degenerate
CC probes designed based on fragments of the purified scavenger receptor
CC protein. The scavenger receptor protein has a binding capacity for
CC acetylated low density lipoprotein (LDL) and binds endotoxin. Fragments
CC of the extracellular portion of the scavenger receptor protein inactivate
CC endotoxin-related substances and are used in the diagnosis and treatment
CC of endotoxaemia. They may be administered to patients at high risk of
CC symptomatic or endotoxic shock. The fragments may also be fixed to inert
CC supports for purification purposes. The fragments may be modified to have
CC greater binding affinity for the endotoxin-related substance than the
CC native scavenger receptor protein, or to more effectively neutralise the
CC toxic or pathogenic effects of moles. that bind the scavenger receptor
CC protein or of organisms which express such moles. See also AAR27035.
CC (Updated on 25-MAR-2003 to correct PN field.)

CC Revised record issued on 23-SEP-2004 : Correction to Feature Table Key

XX Sequence 453 AA;

Query Match 67.1%; Score 1381; DB 2; Length 453;

Best Local Similarity 100.0%; Pred. No. 4.3e-102; Mismatches 0; Gaps 0;

Matches 272; Conservative 0; Indels 0; Gaps 0;

QY 1 MAQWDPDPQOEDTDSCTESVFKDARSVTALIPHPKNGPTLQERMKSYKTLITLYLIV 60
DB 1 MAQWDPDPQOEDTDSCTESVFKDARSVTALIPHPKNGPTLQERMKSYKTLITLYLIV 60
QY 61 FVTVLPITIGIYAAQLKMKETKCTGVSNADISPEBKGKNGSEDEMRPREAVMERMSNM 120
DB 61 FVTVLPITIGIYAAQLKMKETKCTGVSNADISPEBKGKNGSEDEMRPREAVMERMSNM 120
QY 121 ESRIOYLSDNENANLDAKNFQNSITTDORFNDVLFOLNSLLSIOEHENITGDISKSLIV 180
DB 121 ESRIOYLSDNENANLDAKNFQNSITTDORFNDVLFOLNSLLSIOEHENITGDISKSLIV 180
QY 181 GIANTTVLDLQFSIETLNGRVQENAFKQOEEMKLEERLYNASAEIKSLDEKQVYLEOEIK 240
DB 181 GIANTTVLDLQFSIETLNGRVQENAFKQOEEMKLEERLYNASAEIKSLDEKQVYLEOEIK 240
QY 241 GEMKLNITNDRLKDMHESQTLKNITLLQG 272
DB 241 GEMKLNITNDRLKDMHESQTLKNITLLQG 272

RESULT 5

ID AAM19708 standard; protein; 451 AA.

AC AAM19708;

DT 19-AUG-1997 (first entry)

DE Macrophage scavenger receptor protein.

KM Macrophage scavenger receptor protein; MSRP; human; lipoteichoic acid;
KW LTA; Gram-positive bacteria; cell wall; atherosclerosis; host defence;

KM septicemia; inhibitor; complement activation; cytokine release; therapy;
 KM nitric oxide production; bacterial infection; septic shock.
 XX
 OS Homo sapiens.
 XX
 PN US624904-A.
 XX
 PD 29-APR-1997.
 XX
 PF 17-NOV-1993; 93US-00154365.
 XX
 PR 17-NOV-1993; 93US-00154365.
 XX
 PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
 PA (UYVA) UNIV YALE.
 XX
 PI Krieger M, Joiner KA;
 XX
 DR WPI; 1997-258236/23.
 DR N-PSDB; AAT68796.
 XX
 FT Treatment of septicemia caused by Gram-positive bacteria - by
 FT administration of macrophage scavenger receptor protein.
 PS
 PS Disclosure; Col 23-26; 16pp; English.
 XX
 CC This sequence represents the human macrophage scavenger receptor protein
 CC (MSRP). MSRP binds specifically to the lipoteichoic acid (LTA) residues
 CC on the Gram-positive bacterial cell wall. MSRP exhibit unusually broad
 CC binding specificity for polyanionic ligands, and have been implicated in
 CC atherosclerosis and a variety of host defence functions. This protein can
 CC be used in the method of the invention. The method of the invention is
 CC for the treatment of septicemia caused by Gram-positive bacteria. The
 CC method comprises administration of a MSRP in an amount sufficient to
 CC inhibit complement activation, cytokine release or nitric oxide
 CC production induced by LTA released by the Gram-positive bacteria. In
 CC addition to treating Gram-positive septic shock, the MSRP can be used to
 CC screen for other compounds for treating Gram-positive septic shock. MSRP
 CC can also be used to purify, label or detect LTA or LTA-containing cells.
 CC MSRP, active MSRP fragments, anti-MSRP antibodies or other compounds that
 CC inhibit binding of Gram-positive bacteria to MSRP can be used to treat
 CC pathologies such as septicemia, Gram-positive bacterial infection, Gram-
 CC positive septicemia or Gram-positive or Gram-negative septic shock
 CC
 XX
 SO Sequence 451 AA;
 Query Match 50.9%; Score 1047.5; DB 2; Length 451;
 Best Local Similarity 72.5%; Pred. No. 2.7e-75;
 Matches 198; Conservative 40; Mismatches 34; Indels 1; Gaps 1;
 QY 1 MAQMDPDDQOEDTDSCTESYKFPDARSVTALLPPIPKNGPTLOBRMKS YKTALITLYIV 60
 DB 1 MEQMDHFNQOEDTDSCTESYKFPDARSVTALLPPIPKNSPDLDEKLSFKALIALYIV 60
 QY 61 FVVLVPIIGIYVAOQLKMETKNCVGSVNA-DISBPEKGNGSEDEMRPREAVMERMSN 119
 DB 61 FAVLIPILIGIYVAOQLKMETKNCVGSSTNANDITQSLTGKGNDSBEMRFEVMEHMSN 120
 QY 120 MESRIQYISDNEAULDAKNFONFSITTDORFNVLPFANLSSIOGHENITGDISKL 179
 DB 121 MEKRIQHLDMEANLMDTEHFONFSMTDORFNILLQSLTFLSSVOEHENAIDEISKSL 180
 QY 180 VGLNTTVYLDLQFSIETTLNGRVOENAFKQOEMRKLEERIYASAEIKSLDKQVYLEQEI 239
 DB 181 ISLNTTLLDLOLANTENANGKIQENTFKQOERISKLEEVYVVSAEIMAMEGQVHLBEI 240
 QY 240 KGEKMLNNTITNDRLKQMEHSQTLKNITLLQG 272
 DB 241 KGEVYVLIANNITNDRLKQMEHSQTLRNITLLQG 273
 RESULT 6
 ADI62129

ID ADI62129 standard; protein; 451 AA.
 XX
 AC ADI62129;
 XX
 DT 15-APR-2004 (first entry)
 XX
 DE Human macrophage scavenger receptor protein 1 mutant V113A.
 XX
 KM prostate cancer; asthma; cardiovascular disease;
 KM macrophage scavenger receptor protein 1, MSRI; human; receptor; mutant;
 KM mutein.
 XX
 OS Homo sapiens.
 XX
 OS Synthetic.
 XX
 FH Key location/Qualifiers
 FT Misc-difference 113 /note= "Wild type Val substituted by Ala"
 FT
 XX
 PN US2004018521-A1.
 XX
 PD 29-JAN-2004.
 XX
 PP 30-APR-2003; 2003US-00426262.
 XX
 PR 07-MAY-2002; 2002US-0378377P.
 XX
 PA (XUJY/) XU J.
 PA (MEYER/) MEYERS D.
 PA (ZHEN/) ZHENG S.
 PA (WALS/) WALSH P C.
 PA (ISAA/) ISAACS W B.
 PA (BLEE/) BLEECKER E.
 PA (HERR/) HERRINGTON D.
 XX
 PI Xu J, Meyers D, Zheng S, Walsh PC, Isaacs WB, Bleecker E;
 PI Herrington D;
 XX
 DR WPI; 2004-122024/12.
 XX
 FT Screening a subject for increased risk of prostate cancer or asthma, or
 FT decreased risk of cardiovascular disease by detecting the presence or
 FT absence of an MSRI mutation in the subject.
 XX
 PS Claim 1; Page; 21pp; English.
 XX
 CC The invention describes a method of screening a subject for increased
 CC risk of prostate cancer or asthma, or decreased risk of cardiovascular
 CC disease. The method comprises: detecting the presence or absence of an
 CC MSRI mutation in the subject; and determining that the subject is at
 CC increased risk of prostate cancer, increased risk of asthma, or decreased
 CC risk of cardiovascular disease due to the presence or absence of the MSRI
 CC mutation consisting of H441R, G169S, R293X, P275A, D1174Y, V113A, S41Y,
 CC P36A or 154Y. The method is useful for screening a subject for increased
 CC risk of prostate cancer or asthma, or decreased risk of cardiovascular
 CC disease. This is the amino acid sequence of a human macrophage scavenger
 CC protein 1 (MSRI) mutant of the invention. Note: This sequence does not
 CC appear in the printed specification but has been created using
 CC information given in the specification.
 XX
 SO Sequence 451 AA;
 Query Match 50.8%; Score 1046.5; DB 8; Length 451;
 Best Local Similarity 72.5%; Pred. No. 3.3e-75;
 Matches 198; Conservative 41; Mismatches 33; Indels 1; Gaps 1;
 QY 1 MAQMDPDDQOEDTDSCTESYKFPDARSVTALLPPIPKNGPTLOBRMKS YKTALITLYIV 60
 DB 1 MEQMDHFNQOEDTDSCTESYKFPDARSVTALLPPIPKNSPDLDEKLSFKALIALYIV 60
 QY 61 FVVLVPIIGIYVAOQLKMETKNCVGSVNA-DISBPEKGNGSEDEMRPREAVMERMSN 119
 DB 61 FAVLIPILIGIYVAOQLKMETKNCVGSSTNANDITQSLTGKGNDSBEMRFEVMEHMSN 120

QY 120 MESRIQVLSDEANLIDAKNFQNFSTTTDQRFNDVLPQNLSSLOEHENITIGDISKSL 179
 DB 121 MEKRIQHLIDMEANLIDTEHFQNFSTTTDQRFNDILQSLTSPSSVOGHGNAIDETSKSL 180
 QY 180 VGLNTTVLDLQPSIEITLNGRVOENAFKQOEEMRKLEERLYNASAEIKSLDEKQVYLEORI 239
 DB 181 ISLNTTLLDLQNTINENKIQENTFKQOEESKLEERYVNASAEIMAKEQVHLEORI 240
 QY 240 KGEMLNNITNDLRKOMEHSQTLKNITLLQG 272
 DB 241 KGEVAVLNNTINDLRKOMEHSQTLKNITLLQG 273

RESULT 7

AAK21513
 ID AAK21513 standard; protein; 358 AA.
 XX
 AC AAK21513;
 XX
 DT 25-MAR-2003 (revised)
 DT 19-MAY-1992 (first entry)
 XX
 DE Human scavenger receptor type II.
 XX
 KW Lipoproteins.
 XX
 OS Homo sapiens.
 XX
 PN JP03290184-A.
 XX
 PD 19-DEC-1991.
 XX
 PF 06-APR-1990; 90JP-00090274.
 XX
 PR 06-APR-1990; 90JP-00090274.
 XX
 PA (CHUS) CHUGAI PHARM CO LTD.
 DR WPI; 1992-051436/07.
 DR N-PSDB; AAQ21550.
 XX
 PT New scavenger receptor-producing animal cells - which have been
 PT transformed with vector contg. gene for coding human scavenger receptor I
 PT or II type under control of promoter, etc.
 XX
 PS Discloure; Fig 2; 9pp; Japanese.
 CC The gene encoding the receptor can be expressed from a cytomegalo- virus
 CC promoter in a host cell e.g. CHO cell. The resulting recombinant
 CC scavenger receptor can be used to detect modified lipoproteins or
 CC modified substances in the blood. See also AAK21512. (Updated on 25-MAR-
 CC 2003 to correct PA field.)
 CC
 SQ Sequence 358 AA;

Query Match 50.6%; Score 1042.5; DB 2; Length 358;
 Best Local Similarity 72.2%; Pred. No. 4.9e-75;
 Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;

QY 1 MAQWDDPPQOEDTSCSVEKFDARSVTALPPHPKNGPTLOERKSKYKALITLYLV 60
 DB 1 MEQWHFHQQOEDTSCSVEKFDARSMTALPPHPKNSPSLOEKSKKALITLYLV 60
 QY 61 FVVLVPIIGIVAQAOLKMETKNCVGSVNA-DISPSPEKNGSGSEDEMRFREAVMERKSN 119
 DB 61 FAVLLPLIGIVAQAOLKMETKNCVGSVSTVANDITQSLTGKNDSEBERMFOEVMERKSN 120
 QY 120 MESRIQVLSDEANLIDAKNFQNFSTTTDQRFNDVLPQNLSSLOEHENITIGDISKSL 179
 DB 121 MEKRIQHLIDMEANLIDTEHFQNFSTTTDQRFNDILQSLTSPSSVOGHGNAIDETSKSL 180
 QY 180 VGLNTTVLDLQPSIEITLNGRVOENAFKQOEEMRKLEERLYNASAEIKSLDEKQVYLEORI 239

DB 181 ISLNTTLLDLQNTINENKIQENTFKQOEESKLEERYVNASAEIMAKEQVHLEORI 240
 QY 240 KGEMLNNITNDLRKOMEHSQTLKNITLLQG 272
 DB 241 KGEVAVLNNTINDLRKOMEHSQTLKNITLLQG 273

RESULT 8

AAK40803
 ID AAK40803 standard; protein; 358 AA.
 XX
 AC AAK40803;
 XX
 DT 23-FEB-1994 (first entry)
 DT
 XX
 DE Human scavenger receptor II.
 XX
 KW Human; scavenger receptor; antihuman scavenger receptor antibody; AHSRA;
 KW mammal; rabbit; antiserum; monoclonal; HAT-resistant hybridoma;
 KW arteriosclerosis.
 XX
 OS Homo sapiens.
 XX
 PN JP05192179-A.
 XX
 PD 03-AUG-1993.
 XX
 PF 16-AUG-1991; 91JP-00229728.
 XX
 PR 27-AUG-1990; 90JP-00222398.
 XX
 PA (CHUS) CHUGAI PHARM CO LTD.
 DR WPI; 1993-277488/35.
 DR N-PSDB; AAQ47731.
 XX
 PT Anti-human scavenger receptor antibody - useful for monitoring progress
 PT of arteriosclerosis.
 XX
 PS Claim 2; Page 7-9; 10pp; Japanese.
 CC The sequences given in AAK40802-03 represent the human scavenger
 CC receptors I and II. These proteins may be used in the production of
 CC antihuman scavenger receptor antibodies (AHSRA). These peptides were used
 CC to immunise a mammal, pref. a rabbit, and anti-serum was prepared. A
 CC monoclonal antibody was prepared from HAT-resistant hybridoma. These
 CC antibodies may be used to determine the progress of arteriosclerosis
 CC
 SQ Sequence 358 AA;

Query Match 50.6%; Score 1042.5; DB 2; Length 358;
 Best Local Similarity 72.2%; Pred. No. 4.9e-75;
 Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;

QY 1 MAQWDDPPQOEDTSCSVEKFDARSVTALPPHPKNGPTLOERKSKYKALITLYLV 60
 DB 1 MEQWHFHQQOEDTSCSVEKFDARSMTALPPHPKNSPSLOEKSKKALITLYLV 60
 QY 61 FVVLVPIIGIVAQAOLKMETKNCVGSVNA-DISPSPEKNGSGSEDEMRFREAVMERKSN 119
 DB 61 FAVLLPLIGIVAQAOLKMETKNCVGSVSTVANDITQSLTGKNDSEBERMFOEVMERKSN 120
 QY 120 MESRIQVLSDEANLIDAKNFQNFSTTTDQRFNDVLPQNLSSLOEHENITIGDISKSL 179
 DB 121 MEKRIQHLIDMEANLIDTEHFQNFSTTTDQRFNDILQSLTSPSSVOGHGNAIDETSKSL 180
 QY 180 VGLNTTVLDLQPSIEITLNGRVOENAFKQOEEMRKLEERLYNASAEIKSLDEKQVYLEORI 239
 DB 181 ISLNTTLLDLQNTINENKIQENTFKQOEESKLEERYVNASAEIMAKEQVHLEORI 240
 QY 240 KGEMLNNITNDLRKOMEHSQTLKNITLLQG 272

Db 241 KGEVKVILNNTNDLRLKDEHSQTLRNITLLIOG 273

RESULT 9

AAW08078 standard; protein; 358 AA.

AAW08078;

25-FEB-1997 (first entry)

Type II macrophage scavenger receptor.

Type II macrophage scavenger receptor; SRG; kidney; 293 cell;

cell substrate; cell attachment; atherosclerosis.

Homo sapiens.

MO9638725-A1.

05-DEC-1996.

30-MAY-1996; 96WO-US008081.

30-MAY-1995; 95US-00453117.

(SMIK) SMITHKLINE BEECHAM CORP.

Lyoko PG, Elshourbagy NAE, Brawner ME;

WPI; 1997-034505/03.

N-PSDB; AAT43260.

New modified human embryonic kidney 293 cells - transfected with a mammalian scavenger receptor gene to enhance ability to attach to a solid support.

Discloure; Page 16-18; 32pp; English.

Human type I (AAW08077) and type II (AAW08078) macrophage scavenger

receptors can be expressed in human embryonic kidney 293 cells following

transfection of the cells with vectors carrying the respective scavenger

receptor genes (AAT43259 and AAT43260). The transfected cells show an

enhanced ability to attach to a solid support and are useful for

screening cpds. for biological activity, or for identifying antagonists

of the scavenger receptor gene, e.g. to develop agents for treatment of

atherosclerosis

Sequence 358 AA;

Query Match 50.6%; Score 1042.5; DB 2; Length 358;

Best Local Similarity 72.2%; Pred. No. 4.9e-75; Indels 1; Gaps 1;

Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;

1 MAQMDPDPDOEDTDSCTESVYKFDARSVTALLPPHPKNGPTLQERMSYKTALITLYLIY 60

1 MEQMDHFNQOEDTDSCTESVYKFDARSMTALLPPHPKNSPSLQETKSKFKAALTALYLIY 60

61 FVTVLPITIGIYAAOLKMETKCTVGSVNA-DISPSGKNGSGEDKRFREAVMERMSN 119

61 FAVIPLPLIGIYAAOLKMETKCTVGSVNA-DISPSGKNGSGEDKRFREAVMERMSN 120

120 MESRIQYLSDEANLIDAKNFONFSITTDORFNDVLPOLNSLSSIOEHENIIGDISKSL 179

121 MEKRIQHLIDMEANLIDTEHFNFSMTTDORFNDILLOUSTLFSVQGHNAIDELSKSL 180

180 VGLNTTVLDLQFSITELNGRVOENAFKQOEEMKLEERIYNASAEIKSLDEKQYVLEGEI 239

181 ISLNTTLLDLQINENLNGKIQENTFKQOEISKLBERVYNVSAIIMAKEBOVHLEGEI 240

240 KGEKMLNNTNDLRLKDEHSQTLRNITLLIOG 272

241 KGEVKVILNNTNDLRLKDEHSQTLRNITLLIOG 273

RESULT 10

AB49716 standard; protein; 358 AA.

AB49716;

05-APR-2001 (first entry)

Human type II scavenger receptor amino acid sequence.

Human; type II scavenger receptor; antibody; macrophage.

Homo sapiens.

JP2000312595-A.

14-NOV-2000.

16-AUG-1991; 2000JP-00114233.

27-AUG-1990; 90JP-00222398.

16-AUG-1991; 91JP-00229728.

(CHUS) CHUGAI PHARM CO LTD.

WPI; 2001-161981/17.

N-PSDB; AAF29165.

New anti-human scavenger receptor antibody useful for the identification and the determination of macrophages.

Claim 1; Page 7-9; 13pp; Japanese.

This invention relates to a polyclonal or monoclonal antibody which targets a

human type I or type II scavenger receptor epitope. The anti-scavenger

receptor antibody can be used for the identification and determination of

macrophages. The present sequence represents the human type II scavenger

receptor protein, to which the antibody of the invention is directed

Sequence 358 AA;

Query Match 50.6%; Score 1042.5; DB 4; Length 358;

Best Local Similarity 72.2%; Pred. No. 4.9e-75; Indels 1; Gaps 1;

Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;

1 MAQMDPDPDOEDTDSCTESVYKFDARSVTALLPPHPKNGPTLQERMSYKTALITLYLIY 60

1 MEQMDHFNQOEDTDSCTESVYKFDARSMTALLPPHPKNSPSLQETKSKFKAALTALYLIY 60

61 FVTVLPITIGIYAAOLKMETKCTVGSVNA-DISPSGKNGSGEDKRFREAVMERMSN 119

61 FAVIPLPLIGIYAAOLKMETKCTVGSVNA-DISPSGKNGSGEDKRFREAVMERMSN 120

120 MESRIQYLSDEANLIDAKNFONFSITTDORFNDVLPOLNSLSSIOEHENIIGDISKSL 179

121 MEKRIQHLIDMEANLIDTEHFNFSMTTDORFNDILLOUSTLFSVQGHNAIDELSKSL 180

180 VGLNTTVLDLQFSITELNGRVOENAFKQOEEMKLEERIYNASAEIKSLDEKQYVLEGEI 239

181 ISLNTTLLDLQINENLNGKIQENTFKQOEISKLBERVYNVSAIIMAKEBOVHLEGEI 240

240 KGEKMLNNTNDLRLKDEHSQTLRNITLLIOG 272

241 KGEVKVILNNTNDLRLKDEHSQTLRNITLLIOG 273

RESULT 11

AD889003 standard; protein; 358 AA.

AD889003;

[illegible]

Qy	180	VGANTLVLLDQSIETLRNVOENFVKQOEKRLKEETIVASAEISLSEKQVYLQEI	234
Dd	181	ISANTLVLLDQANTENLNKQIIDENTFFKQOEISKLSEKRVVNSAEINAMKEQVHLEQEI	240
Qy	240	KGEKMLNNITNDLRKDKWEHSQTLKNITLLQG	272
Dd	241	KGEVKVNNITNDLRKDKWEHSQTLKNITLLQG	273
RESULT 12			
ADQ39735		standard; protein; 358 AA.	
ADQ39735			
ADQ39735			
18-NOV-2004		(first entry)	
Dd		Human myocardial infarction-associated gene derived protein, SEQ ID 1398	
De		Myocardial infarction; detection; single nucleotide polymorphism; SNP;	
KM		cardiant; gene therapy; human.	
XX			
OS		Homo sapiens.	
XX			
PD		MO2004058052-A2.	
PN		15-JUL-2004.	
XX			
PP		22-DEC-2003; 2003WO-US040978.	
PR		20-DEC-2002; 2002US-0434778P.	
PR		10-MAR-2003; 2003US-0453135P.	
PR		30-APR-2003; 2003US-0466412P.	
PR		23-SEP-2003; 2003US-0504955P.	
XX			
PA		(APPL-) APPLERA CORP.	
XX			
PI		Cargill M, Devlin JJ, Iakoubova O;	
XX			
DR		NPI, 2004-533949/51.	
XX		N-PDB; ADQ38907.	
PT			
PT		Identifying an individual who has an altered risk for developing	
PT		myocardial infarction by detecting a single nucleotide polymorphism in	
PT		the individual's nucleic acids.	
PS		Claim 10; SEQ ID NO 1398; 145pp; English.	
XX			
XX			
CC		The invention relates to a novel method for identifying an individual who	
CC		has an altered risk for developing myocardial infarction. The method	
CC		comprises detecting a single nucleotide polymorphism (SNP) in any one of	
CC		the nucleotide sequences given in the specification in the individual's	
CC		nucleic acids, where the presence of the SNP is correlated with an	
CC		altered risk for myocardial infarction in the individual. The invention	
CC		further comprises: an isolated nucleic acid molecule comprising at least	
CC		8 contiguous nucleotides where one of the nucleotides is an SNP given in	
CC		the specification or its complement and encoding any one of the amino	
CC		acid sequences given in the specification; an isolated polypeptide	
CC		comprising an amino acid sequence given in the specification; an antibody	
CC		that specifically binds to the polypeptide or its antigen-binding	
CC		fragment; an amplified polynucleotide containing an SNP given in the	
CC		specification and which is between about 16 and 1000 nucleotides in	
CC		length; a kit for detecting an SNP in a nucleic acid, comprising the	
CC		polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a	
CC		nucleic acid molecule; a method of detecting a variant polypeptide; and a	
CC		method for identifying an agent useful in treating or preventing	
CC		myocardial infarction. The novel detection method has cardiant activity.	
CC		The nucleic acids of the invention may be used in gene therapy. The	
CC		method is useful in identifying an individual who has an increased or	
CC		decreased risk for developing myocardial infarction and for preparing a	
CC		composition for treating or preventing myocardial infarction. This	
CC		sequence represents the protein of a human myocardial infarction-	

CC associated gene containing one or more SNPs of the invention. Note: This
CC sequence was not shown in the specification. The sequence has come from
CC an electronic sequence listing downloaded from the WIPO website.

XX Sequence 358 AA;

Query Match 50.6%; Score 1042.5; DB 8; Length 358;
Best Local Similarity 72.2%; Pred. No. 4.9e-75;
Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;

QY 1 MAQWDDPDDQEDDCTESVYKPDARSVTALLPFPKNGPTLQERMSYKATLITLYLIY 60

DB 1 MEQWDHFNQOEDDSDSESVKFPDARSMTALLPFPKNGSPSLQKLSFKKALITLYLIY 60

QY 61 FVVLVPIIIGVAAQLLWETKNCVGSVNA-DISPSPGKNGSEDEMRFPFVEMERHSN 119

DB 61 FAVLIPILIGVAAQLLWETKNCVGSVNA-DISPSPGKNGSEDEMRFPFVEMERHSN 120

QY 120 MESRIQYLSDEANILLAKNFQNFSTTDOGFNVLFQNLNLSIOEHENIIGDISKSL 179

DB 121 MEKRIQHLDEANILLMDTEHFQNFSTTDOGFNILLQSLTSPSVQGHGNAIDKSL 180

QY 180 VGLNTTVLDLQFSIETLNGRVOENAFKQOEBMRKLEERIVNASAEIKSLDEKQVYLEGEI 239

DB 181 ISLNTTLLDLQNLNENLNGKIQENTFKQOEISKLEERVYVNSAEMKKEQVHLEGEI 240

QY 240 KGEVKVLNNTITNDRLKDWHSQTLRNITLLQG 272

DB 241 KGEVKVLNNTITNDRLKDWHSQTLRNITLLQG 273

RESULT 13

ADQ39731 standard; protein; 358 AA.

XX ADQ39731;

DT 18-NOV-2004 (first entry)

XX Human myocardial infarction-associated gene derived protein, SEQ ID 1394.

XX Myocardial infarction; detection; single nucleotide polymorphism; SNP;

XX cardiant; gene therapy; human.

XX Homo sapiens.

XX WO2004058052-A2.

XX 15-JUL-2004.

XX 22-DEC-2003; 2003WO-US040978.

XX 20-DEC-2002; 2002US-0434778P.

XX 10-MAR-2003; 2003US-045135P.

XX 30-APR-2003; 2003US-046412P.

XX 23-SEP-2003; 2003US-0504955P.

XX (APPL-) APPLERA CORP.

XX Cargill M, Devlin J, Iakubova O;

XX WPI; 2004-533949/51.

XX N-PSDB; ADQ38903.

XX Identifying an individual who has an altered risk for developing

XX myocardial infarction by detecting a single nucleotide polymorphism in

XX the individual's nucleic acids.

XX Claim 10; SEQ ID NO 1394; 145pp; English.

XX The invention relates to a novel method for identifying an individual who

XX has an altered risk for developing myocardial infarction. The method

XX comprises detecting a single nucleotide polymorphism (SNP) in any one of

CC the nucleotide sequences given in the specification in the individual's

CC nucleic acids, where the presence of the SNP is correlated with an

CC altered risk for myocardial infarction in the individual. The invention

CC further comprises: an isolated nucleic acid molecule comprising at least

CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in

CC the specification or its complement and encoding any one of the amino

CC acid sequences given in the specification; an isolated polypeptide

CC comprising an amino acid sequence given in the specification; an antibody

CC that specifically binds to the polypeptide or its antigen-binding

CC fragment; an amplified polynucleotide containing an SNP given in the

CC specification and which is between about 16 and 1000 nucleotides in

CC length; a kit for detecting an SNP in a nucleic acid, comprising the

CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a

CC nucleic acid molecule; a method of detecting a variant polypeptide; and a

CC method for identifying an agent useful in treating or preventing

CC myocardial infarction. The novel detection method has cardiant activity.

CC The nucleic acids of the invention may be used in gene therapy. The

CC method is useful in identifying an individual who has an increased or

CC decreased risk for developing myocardial infarction and for preparing a

CC composition for treating or preventing myocardial infarction. This

CC sequence represents the protein of a human myocardial infarction-

CC associated gene containing one or more SNPs of the invention. Note: This

CC sequence was not shown in the specification. The sequence has come from

CC an electronic sequence listing downloaded from the WIPO website.

XX Sequence 358 AA;

Query Match 50.6%; Score 1042.5; DB 8; Length 358;
Best Local Similarity 72.2%; Pred. No. 4.9e-75;
Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;

QY 1 MAQWDDPDDQEDDCTESVYKPDARSVTALLPFPKNGPTLQERMSYKATLITLYLIY 60

DB 1 MEQWDHFNQOEDDSDSESVKFPDARSMTALLPFPKNGSPSLQKLSFKKALITLYLIY 60

QY 61 FVVLVPIIIGVAAQLLWETKNCVGSVNA-DISPSPGKNGSEDEMRFPFVEMERHSN 119

DB 61 FAVLIPILIGVAAQLLWETKNCVGSVNA-DISPSPGKNGSEDEMRFPFVEMERHSN 120

QY 120 MESRIQYLSDEANILLAKNFQNFSTTDOGFNVLFQNLNLSIOEHENIIGDISKSL 179

DB 121 MEKRIQHLDEANILLMDTEHFQNFSTTDOGFNILLQSLTSPSVQGHGNAIDKSL 180

QY 180 VGLNTTVLDLQFSIETLNGRVOENAFKQOEBMRKLEERIVNASAEIKSLDEKQVYLEGEI 239

DB 181 ISLNTTLLDLQNLNENLNGKIQENTFKQOEISKLEERVYVNSAEMKKEQVHLEGEI 240

QY 240 KGEVKVLNNTITNDRLKDWHSQTLRNITLLQG 272

DB 241 KGEVKVLNNTITNDRLKDWHSQTLRNITLLQG 273

RESULT 14

ADQ39734 standard; protein; 358 AA.

XX ADQ39734;

DT 18-NOV-2004 (first entry)

XX Human myocardial infarction-associated gene derived protein, SEQ ID 1397.

XX Myocardial infarction; detection; single nucleotide polymorphism; SNP;

XX cardiant; gene therapy; human.

XX Homo sapiens.

XX WO2004058052-A2.

XX 15-JUL-2004.

XX 22-DEC-2003; 2003WO-US040978.

20-DEC-2002; 2002US-0434778P.
 10-MAR-2003; 2003US-0453135P.
 30-APR-2003; 2003US-0466412P.
 23-SEP-2003; 2003US-0504955P.

(APPL-) APPLERA CORP.

Cargill M, Devlin J, Iakubova O;

WPI; 2004-533949/51.

N-PSDB; ADQ38906.

Identifying an individual who has an altered risk for developing myocardial infarction by detecting a single nucleotide polymorphism in the individual's nucleic acids.

Claim 10; SEQ ID NO 1397; 145bp; English.

The invention relates to a novel method for identifying an individual who has an altered risk for developing myocardial infarction. The method comprises detecting a single nucleotide polymorphism (SNP) in any one of the nucleotide sequences given in the specification in the individual's nucleic acids, where the presence of the SNP is correlated with an altered risk for myocardial infarction in the individual. The invention further comprises: an isolated nucleic acid molecule comprising at least 8 contiguous nucleotides where one of the nucleotides is an SNP given in the specification or its complement and encoding any one of the amino acid sequences given in the specification; an isolated polypeptide comprising an amino acid sequence given in the specification; an antibody that specifically binds to the polypeptide or its antigen-binding fragment; an amplified polynucleotide containing an SNP given in the specification and which is between about 16 and 1000 nucleotides in length; a kit for detecting an SNP in a nucleic acid, comprising the polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a nucleic acid molecule; a method of detecting a variant polypeptide; and a method for identifying an agent useful in treating or preventing myocardial infarction. The novel detection method has cardiac activity. The nucleic acids of the invention may be used in gene therapy. The method is useful in identifying an individual who has an increased or decreased risk for developing myocardial infarction and for preparing a composition for treating or preventing myocardial infarction. This sequence represents the protein of a human myocardial infarction-associated gene containing one or more SNPs of the invention. Note: This sequence was not shown in the specification. The sequence has come from an electronic sequence listing downloaded from the WIPO website.

Sequence 358 AA;

Query Match 50.6%; Score 1042.5; DB 8; Length 358;

Best Local Similarity 72.2%; Pred. No. 4.9e-75; Mismatches 34; Indels 1; Gaps 1;

Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;

1 MAOWDPDPOQEDTDSCTESVFPDARSVALPPEPKNGPTQOERMSKYKALITLYLIV 60
 1 MEQWDFHFNQOEDTDSCTESVFPDARSVALPPEPKNGPTQOERMSKYKALITLYLIV 60
 61 FVVLVPIIGIYVAQAOLKMKETKCTGVSVA-DISSPBEKKGSGEDENRFRFAVMERN 119
 61 FAVLPLGIYVAQAOLKMKETKCTGVSVA-DISSPBEKKGSGEDENRFRFAVMERN 120
 120 MESRIQVSDNEANLDAKNPFSITTDORFNDVLPOLNLSLSIOEHENITIGISKL 179
 121 MEKRIQVSDNEANLDAKNPFSITTDORFNDVLPOLNLSLSIOEHENITIGISKL 180
 180 VGLNTVLDLQPSITLGRVQENAFKQOERMKLEBRLYNNAASIKSLDEKQVYLBORI 239
 181 ISLNTTLDLQPSITLGRVQENAFKQOERMKLEBRLYNNAASIKSLDEKQVYLBORI 240
 240 KGEMLANNITNDLAKMEHSQTKNTLLQG 272
 241 KGEVYVANNITNDLAKMEHSQTKNTLLQG 273

RESULT 15

ADQ39733

ID ADQ39733 standard; protein; 388 AA.

ADQ39733;

18-NOV-2004 (first entry)

Human myocardial infarction-associated gene derived protein, SEQ ID 1396.

Myocardial infarction; detection; single nucleotide polymorphism; SNP;

cardiac; gene therapy; human.

Homo sapiens.

WO2004058052-A2.

15-JUL-2004.

22-DEC-2003; 2003WO-US040978.

20-DEC-2002; 2002US-0434778P.

10-MAR-2003; 2003US-0453135P.

30-APR-2003; 2003US-0466412P.

23-SEP-2003; 2003US-0504955P.

(APPL-) APPLERA CORP.

Cargill M, Devlin J, Iakubova O;

WPI; 2004-533949/51.

N-PSDB; ADQ38906.

Identifying an individual who has an altered risk for developing myocardial infarction by detecting a single nucleotide polymorphism in the individual's nucleic acids.

Claim 10; SEQ ID NO 1396; 145bp; English.

The invention relates to a novel method for identifying an individual who has an altered risk for developing myocardial infarction. The method comprises detecting a single nucleotide polymorphism (SNP) in any one of the nucleotide sequences given in the specification in the individual's nucleic acids, where the presence of the SNP is correlated with an altered risk for myocardial infarction in the individual. The invention further comprises: an isolated nucleic acid molecule comprising at least 8 contiguous nucleotides where one of the nucleotides is an SNP given in the specification or its complement and encoding any one of the amino acid sequences given in the specification; an isolated polypeptide comprising an amino acid sequence given in the specification; an antibody that specifically binds to the polypeptide or its antigen-binding fragment; an amplified polynucleotide containing an SNP given in the specification and which is between about 16 and 1000 nucleotides in length; a kit for detecting an SNP in a nucleic acid, comprising the polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a nucleic acid molecule; a method of detecting a variant polypeptide; and a method for identifying an agent useful in treating or preventing myocardial infarction. The novel detection method has cardiac activity. The nucleic acids of the invention may be used in gene therapy. The method is useful in identifying an individual who has an increased or decreased risk for developing myocardial infarction and for preparing a composition for treating or preventing myocardial infarction. This sequence represents the protein of a human myocardial infarction-associated gene containing one or more SNPs of the invention. Note: This sequence was not shown in the specification. The sequence has come from an electronic sequence listing downloaded from the WIPO website.

Sequence 388 AA;

Query Match 50.6%; Score 1042.5; DB 8; Length 388;

Best Local Similarity 72.2%; Pred. No. 5.5e-75; Mismatches 34; Indels 1; Gaps 1;

Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;

Qy	1	MACWDDPDDQEDPTDSCSYKFDARSVTALLPPHKNQPTLOERMKSXTALITLYLIV	60
Db	1	MEQMDHFHQOEDPTDSCSESYPDARSMTALLPPNPKNSPDLQEKLSFKALALALYLV	60
Qy	61	FVVLVPIIGIIVAQOLKMETNCTVGSVNA-DISPSPEKGNGSEDEMRPREAVMERNSN	119
Db	61	FAVLIPILIGIIVAQOLKMETNCTVGSSTNANDITQSLTGKGNDSHEEMRFQEVFMEHNSN	120
Qy	120	MESRIQYLSDEANLILDAKNFONFSITTDORFNDVLPOLNSLSSIOEHENIIGDISKSL	179
Db	121	MEKRIQHILDEANLIMDTHEFPONFSMTDORFNDILQLSTLFSSVOGHGNAIDDISKSL	180
Qy	180	VGLNTTVLLOFSIETTLNGRVOENAFKQOEMRKLEERIVNASAEIKSLDERKOYVLEQEI	239
Db	181	ISLNTTLLDLQJNIENTNGKIQENTFKQOEISKLEERVYVNSAEIMAKMEQVHLBQEI	240
Qy	240	KGEMKLNNITNDLRLKDMESHQTLKNITLLQG	272
Db	241	KGEVKVNLNITNDLRLKDMESHQTLRNITLLQG	273

Search completed: February 16, 2006, 17:01:04
 Job time : 189 secs

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OM protein - protein search, using sw model

Run on: February 16, 2006, 17:01:22 ; Search time 40 Seconds
(without alignment)
962.168 Million cell updates/sec

Title: US-10-618-570-2

Perfect score: 2059

Sequence: 1 MAQMDPFDQOEDTDSCTES.....DKATRGVGINFTRLRTQKE 400

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1381	67.1	349	2 S08278	macrophage scaveng
2	1381	67.1	453	2 S08276	macrophage scaveng
3	1042.5	50.6	358	2 B38415	macrophage scaveng
4	1042.5	50.6	451	2 A38415	macrophage scaveng
5	994.5	48.3	454	2 A44407	macrophage scaveng
6	987.5	48.0	354	2 I46862	macrophage scaveng
7	987.5	48.0	454	2 I46862	macrophage scaveng
8	801	38.9	350	2 I73338	macrophage scaveng
9	801	38.9	458	2 B44407	macrophage scaveng
10	678	33.9	152	1 V1CH	avidin precursor
11	491	22.8	150	2 S42204	avidin-related pro
12	461	22.4	150	2 S42203	avidin-related pro
13	452	22.0	150	2 S42201	avidin-related pro
14	436	21.2	150	2 S42202	avidin-related pro
15	140	6.8	1064	2 A40136	fibropilin Ia - s
16	139.5	6.8	183	2 S57285	streptavidin v2 pr
17	138.5	6.7	183	2 S57284	streptavidin v1 pr
18	138.5	6.7	183	2 A23513	streptavidin precu
19	133.5	6.5	715	2 C70174	methyl-accepting c
20	133.5	6.4	570	2 H97244	membrane associate
21	132.5	6.4	1163	2 G97236	ATPase involved in
22	129.5	6.3	702	2 P97352	CGI protein - huma
23	129.5	6.3	1300	2 I53799	hypothetical prote
24	128.5	6.2	802	2 E91210	hypothetical prote
25	128.5	6.2	802	2 H86056	hypothetical prote
26	128	6.2	833	2 H72205	maltoase ABC transp
27	127.5	6.1	1127	2 T28317	ORF MSV156 hypothe
28	126.5	6.1	956	2 S30834	hypothetical prote
29	126	6.1	1410	1 A57013	early endosome ant

30	124.5	6.0	572	2 T34273	hypothetical prote
31	124.5	6.0	821	2 S67087	hypothetical prote
32	124	6.0	570	2 A48836	fibropilin C prec
33	123.5	6.0	742	2 UC7595	scavenger receptor
34	123.5	6.0	1156	2 B70356	chromosome assembl
35	123	6.0	1009	2 C89910	hypothetical prote
36	123	6.0	2663	1 S28261	centromere protein
37	122.5	5.9	697	2 D84429	hypothetical prote
38	122	5.9	609	2 S46019	YSM1 protein - yea
39	121.5	5.9	320	2 B97206	methyl-accepting c
40	121	5.9	659	2 G82365	methyl-accepting c
41	121	5.9	667	2 B97012	methyl-accepting c
42	120	5.8	1356	2 S3763	kinectin 1 - human
43	119.5	5.8	570	2 A97238	membrane associate
44	119.5	5.8	908	2 AH0055	probable cation-tr
45	119.5	5.8	1265	2 T47626	structural mainten

ALIGNMENTS

RESULT 1

S08278
macrophage scavenger receptor, splice form II - bovine
N:Alternate names: macrophage scavenger receptor type II
C:Species: Bos primigenius taurus (cattle)
C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C:Accession: S08278
R:Rohter, L.; Freeman, M.; Kodama, T.; Penman, M.; Krieger, M.
Nature 343, 570-572, 1990
A:Title: Coiled-coil fibrous domains mediate ligand binding by macrophage scavenger rece
A:Reference number: S08278; MUID:90136973; PMID:2300208
A:Accession: S08278

A:Molecule type: mRNA
A:Status: not compared with conceptual translation
A:Residues: 1-349 <ROH>
A:Cross-references: UNIPROT:P21758; UNIPARC:UP1000002A6E2; GB:X54183; NID:G736; PIDN:CA
C:Keywords: alternative splicing; coiled coil; glycoprotein; transmembrane protein
F:51-76/Domain: transmembrane #status predicted <TM>
F:82,101,142,183,220,248,266/Binding site: carbohydrate (Aan) (covalent) #status predict

Query Match 67.1%; Score 1381; DB 2; Length 349;

Best Local Similarity 100.0%; Pred.No. 2.8e-79; Matches 272; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MAQMDPFDQOEDTDSCTESVFPDARSTALLPFPKXGPTLQERKSKYKTLITLYLV 60
DB	1	MAQMDPFDQOEDTDSCTESVFPDARSTALLPFPKXGPTLQERKSKYKTLITLYLV 60
QY	61	FVVLVPIIGIYVAOLLLKMKETKCTVGSVNAADISPEGKNGSEDEMRPREAVMERMSNM 120
DB	61	FVVLVPIIGIYVAOLLLKMKETKCTVGSVNAADISPEGKNGSEDEMRPREAVMERMSNM 120
QY	121	BSRIQYLSDNENANLLDANKFONFSITTDQRFNDVLFOUNLSLSSIOEHENITGDISKSLV 180
DB	121	BSRIQYLSDNENANLLDANKFONFSITTDQRFNDVLFOUNLSLSSIOEHENITGDISKSLV 180
QY	181	GIANTTVLDQFSIETLNGRVQENAFKQOEENKLEERLYNAAETKSLDEKQVYLEQETK 240
DB	181	GIANTTVLDQFSIETLNGRVQENAFKQOEENKLEERLYNAAETKSLDEKQVYLEQETK 240
QY	241	GEMKLLNNTINDLRKQWEHSQTLLKNITLLQG 272
DB	241	GEMKLLNNTINDLRKQWEHSQTLLKNITLLQG 272

RESULT 2

S08276
macrophage scavenger receptor, splice form I - bovine
N:Alternate names: macrophage scavenger receptor type I
C:Species: Bos primigenius taurus (cattle)
C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C:Accession: S08276

R:Kodama, T.; Freeman, M.; Rohrer, L.; Zabrecky, J.; Matsudaite, P.; Krieger, M.
 Nature 343, 531-535, 1990
 A:Title: Type I macrophage scavenger receptor contains alpha-helical and collagen-like c
 A:Reference number: S08276; MUID:90136665; PMID:2300204
 A:Accession: S08276
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-453 <KOD>
 A:Cross-references: UNIPROT:p21758; UNIPARC:UPI000012F685; GB:X51689; GB:X54182; NID:G73
 A:Note: part of this sequence was confirmed by protein sequencing
 C:Superfamily: macrophage scavenger receptor; scavenger receptor cysteine-rich domain hc
 C:Keywords: alternative splicing; coiled coil; glycoprotein; transmembrane protein
 F:51-76/Domain: transmembrane #status predicted <TM>
 F:349-452/Domain: scavenger receptor cysteine-rich domain homology <SRC>
 F:82,101,142,183,220,248,266/Binding site: carbohydrate (Aan) (covalent) #status predict

Query Match 67.1%; Score 1381; DB 2; Length 453;
 Best Local Similarity 100.0%; Pred. No. 4e-79;
 Matches 272; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAOMDDPDDQEDDSDCTESVYKFDARSVTALLPFPKNGPTLOBRMSKYKTALITLYIV 60
 Db 1 MAOMDDPDDQEDDSDCTESVYKFDARSVTALLPFPKNGPTLOBRMSKYKTALITLYIV 60
 Qy 61 FVLVPIIIGIYAAQLKMKETKCTVGSVNADISPSPEKNGSEDEMRFREAVMERMSN 120
 Db 61 FVLVPIIIGIYAAQLKMKETKCTVGSVNADISPSPEKNGSEDEMRFREAVMERMSN 120
 Qy 121 ESRIOYLSDEANLIDAKNFQNSITTDQRFNDVLPOLNSLSSIOEHENITGDISKSLV 180
 Db 121 ESRIOYLSDEANLIDAKNFQNSITTDQRFNDVLPOLNSLSSIOEHENITGDISKSLV 180
 Qy 121 ESRIOYLSDEANLIDAKNFQNSITTDQRFNDVLPOLNSLSSIOEHENITGDISKSLV 180
 Db 121 ESRIOYLSDEANLIDAKNFQNSITTDQRFNDVLPOLNSLSSIOEHENITGDISKSLV 180
 Qy 181 GLNTTVLDLQFSIETLNGRVOENAFKQOEEMRKLEERYLYNSAEIKSLDEKQVYLEOEIK 240
 Db 181 GLNTTVLDLQFSIETLNGRVOENAFKQOEEMRKLEERYLYNSAEIKSLDEKQVYLEOEIK 240
 Qy 241 GEMKLNNTITNDLRKDWESQTLKNITTLQ 272
 Db 241 GEMKLNNTITNDLRKDWESQTLKNITTLQ 272

RESULT 3
 B38415
 A:Title: macrophage scavenger receptor, splice form II - human
 C:Species: Homo sapiens (man)
 C:Date: 28-Jun-1991 #sequence_revision 28-Jun-1991 #text_change 09-Jul-2004
 C:Accession: B38415
 R:Macumoto, A.; Naito, M.; Itakura, H.; Ikemoto, S.; Asaoka, H.; Hayakawa, I.; Kanamori
 man, D.B.; Kodama, T.
 Proc. Natl. Acad. Sci. U.S.A. 87, 9133-9137, 1990
 A:Title: Human macrophage scavenger receptors: primary structure, expression, and local
 A:Reference number: A38415; MUID:91067661; PMID:2251254
 A:Accession: B38415
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-358 <MAT>
 A:Cross-references: UNIPROT:p21757; UNIPARC:UPI000002AE63; GB:D90188; NID:G219991; PIDN:
 C:Comment: For an alternative splice form, see PIR:A38415.
 C:Genetics:
 A:Gene: GDB:MSR1
 A:Cross-references: GDB:128046; OMIM:153622
 A:Map position: 8p22-8p22
 C:Superfamily: macrophage scavenger receptor; scavenger receptor cysteine-rich domain hc
 C:Keywords: alternative splicing; coiled coil; transmembrane protein

Query Match 50.6%; Score 1042.5; DB 2; Length 358;
 Best Local Similarity 72.2%; Pred. No. 4.5e-58;
 Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;

Qy 1 MAOMDDPDDQEDDSDCTESVYKFDARSVTALLPFPKNGPTLOBRMSKYKTALITLYIV 60
 Db 1 MAOMDDPDDQEDDSDCTESVYKFDARSVTALLPFPKNGPTLOBRMSKYKTALITLYIV 60

Qy 61 FVLVPIIIGIYAAQLKMKETKCTVGSVNA-DISPSPEKNGSEDEMRFREAVMERMSN 119
 Db 61 FVLVPIIIGIYAAQLKMKETKCTVGSVNA-DISPSPEKNGSEDEMRFREAVMERMSN 120
 Qy 120 MESRIOYLSDEANLIDAKNFQNSITTDQRFNDVLPOLNSLSSIOEHENITGDISKSL 179
 Db 120 MESRIOYLSDEANLIDAKNFQNSITTDQRFNDVLPOLNSLSSIOEHENITGDISKSL 180
 Qy 180 VGLNTTVLDLQFSIETLNGRVOENAFKQOEEMRKLEERYLYNSAEIKSLDEKQVYLEOEI 239
 Db 180 VGLNTTVLDLQFSIETLNGRVOENAFKQOEEMRKLEERYLYNSAEIKSLDEKQVYLEOEI 240
 Qy 240 KGEKLNNTITNDLRKDWESQTLKNITTLQ 272
 Db 240 KGEKLNNTITNDLRKDWESQTLKNITTLQ 273

RESULT 4
 A38415
 A:Title: macrophage scavenger receptor, splice form I - human
 C:Species: Homo sapiens (man)
 C:Date: 28-Jun-1991 #sequence_revision 28-Jun-1991 #text_change 09-Jul-2004
 C:Accession: A38415; A4408
 R:Macumoto, A.; Naito, M.; Itakura, H.; Ikemoto, S.; Asaoka, H.; Hayakawa, I.; Kanamori
 man, D.B.; Kodama, T.
 Proc. Natl. Acad. Sci. U.S.A. 87, 9133-9137, 1990
 A:Title: Human macrophage scavenger receptors: primary structure, expression, and local
 A:Reference number: A38415; MUID:91067661; PMID:2251254
 A:Accession: A38415
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-451 <MAT>
 A:Cross-references: UNIPROT:p21757; UNIPARC:UPI000012F686; GB:D90187; NID:G219989; PIDN:
 R:Emi, M.; Asaoka, H.; Matsumoto, A.; Itakura, H.; Kurihara, Y.; Wada, Y.; Kanamori, H.;
 J. Biol. Chem. 268, 2120-2125, 1993
 A:Title: Structure, organization, and chromosomal mapping of the human macrophage scaven
 A:Reference number: A4408; MUID:93131971; PMID:8093617
 A:Accession: A4408
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: nucleic acid
 A:Residues: 155-272 <EMI>
 A:Cross-references: UNIPARC:UPI0000176ED4
 A:Note: sequence extracted from NCBI backbone (NCBI:P123189)
 C:Comment: For an alternative splice form, see PIR:B38415.
 C:Genetics:
 A:Gene: GDB:MSR1
 A:Cross-references: GDB:128046; OMIM:153622
 A:Map position: 8p22-8p22
 C:Superfamily: macrophage scavenger receptor; scavenger receptor cysteine-rich domain ho
 C:Keywords: alternative splicing; coiled coil; transmembrane protein
 F:347-450/Domain: scavenger receptor cysteine-rich domain homology <SRC>

Query Match 50.6%; Score 1042.5; DB 2; Length 451;
 Best Local Similarity 72.2%; Pred. No. 6.1e-58;
 Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;

Qy 1 MAOMDDPDDQEDDSDCTESVYKFDARSVTALLPFPKNGPTLOBRMSKYKTALITLYIV 60
 Db 1 MAOMDDPDDQEDDSDCTESVYKFDARSVTALLPFPKNGPTLOBRMSKYKTALITLYIV 60
 Qy 61 FVLVPIIIGIYAAQLKMKETKCTVGSVNA-DISPSPEKNGSEDEMRFREAVMERMSN 119
 Db 61 FVLVPIIIGIYAAQLKMKETKCTVGSVNA-DISPSPEKNGSEDEMRFREAVMERMSN 120
 Qy 120 MESRIOYLSDEANLIDAKNFQNSITTDQRFNDVLPOLNSLSSIOEHENITGDISKSL 179
 Db 120 MESRIOYLSDEANLIDAKNFQNSITTDQRFNDVLPOLNSLSSIOEHENITGDISKSL 180
 Qy 180 VGLNTTVLDLQFSIETLNGRVOENAFKQOEEMRKLEERYLYNSAEIKSLDEKQVYLEOEI 239
 Db 180 VGLNTTVLDLQFSIETLNGRVOENAFKQOEEMRKLEERYLYNSAEIKSLDEKQVYLEOEI 240
 Qy 240 KGEKLNNTITNDLRKDWESQTLKNITTLQ 272
 Db 240 KGEKLNNTITNDLRKDWESQTLKNITTLQ 272

Db 241 KGEVAVLNITNDLRLKQWHSQTLRNITLIG 273

RESULT 5

A44407

macrophage scavenger receptor, splice form II - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C>Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 15-Oct-1999

C:Accession: A44407

R:Doi, T.; Higashino, K.; Kurihara, Y.; Wada, Y.; Miyazaki, T.; Nakamura, H.; Uesugi, S.

J. Biol. Chem. 268, 2126-2133, 1993

A:Title: Charged collagen structure mediates the recognition of negatively charged macro

A:Reference number: A44407; PMID:93131972; PMID:9380589

A:Accession: A44407

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-454 <DOI>

A:Cross-references: UNIPARC:UPI0000176BD3

A:Experimental source: lung

A:Note: Sequence extracted from NCBI backbone (NCBIP:123206)

C:Superfamily: macrophage scavenger receptor; scavenger receptor cysteine-rich domain ho

C:Keywords: alternative splicing

F:350-453/Domain: scavenger receptor cysteine-rich domain homology <SRC>

Query Match 48.3%; Score 994.5; DB 2; Length 454;

Best Local Similarity 69.2%; Pred. No. 6.2e-55;

Matches 189; Conservative 44; Mismatches 39; Indels 1; Gaps 1;

Db 1 MAQMDPFDQEDTSCSSEVYFDRASVTALLPPHPKNGPTLOERKSKYKALITLYLIV 60

1 MAQMSFTDQEDTSCSSEVYFDRASVTALLPPHPKNGPTLOERKSKYKALITLYLIV 60

Qy 61 FVVLVPIIGIYAAQLKMETKCTVGSVNAD-ISPSPGKNGSGSDENKFRFAVNERMSN 119

61 FAVLPITAIIMAAQLKMKMCKCTGSIANSVSSLLGRGNDSEBEVAFREVMHEHSK 120

Qy 120 MESRIQYISDNEANLLDAKNFQNSITTDQRENDVLFQNLSSLSIOEHENIIGISKSL 179

121 MEKRIQYISDNEANLLDAKNFQNSITTDQRENDVLFQNLSSLSIOEHENIIGISKSL 180

Qy 180 VGLNTTVLDLPISITLNGRVOENAFKQOEKREKLEERLYNNAASAIKSIDEKQVYLEOEI 239

181 ISLNTTLLDLHLVETLVNFKFQENTLKQGEETSKLERVHNASAEIMSKKEQVHLEOEI 240

Qy 240 KGEMLNNITNDLRLKQWHSQTLRNITLIG 272

241 KREAVLNITNDLRLKQWHSQTLRNITLIG 273

Db 241 KREAVLNITNDLRLKQWHSQTLRNITLIG 273

RESULT 6

146863

macrophage scavenger receptor, splice form II - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C>Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 09-Jul-2004

C:Accession: I46863

R:Bickel, P.E.; Freeman, M.W.

J. Clin. Invest. 90, 1450-1457, 1992

A:Title: Rabbit aortic smooth muscle cells express inducible macrophage scavenger recept

A:Reference number: I46863; PMID:93016877; PMID:1401078

A:Accession: I46863

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-354 <BIC>

A:Cross-references: UNIPROT:Q05585; UNIPARC:UPI000002AB64; GB:U11692; NID:G165510; PIN:

C:Superfamily: macrophage scavenger receptor; scavenger receptor cysteine-rich domain ho

C:Keywords: alternative splicing

Query Match 48.0%; Score 987.5; DB 2; Length 354;

Best Local Similarity 68.9%; Pred. No. 1.2e-54;

Matches 188; Conservative 44; Mismatches 40; Indels 1; Gaps 1;

Qy 1 MAQMDPFDQEDTSCSSEVYFDRASVTALLPPHPKNGPTLOERKSKYKALITLYLIV 60

Db 1 MAQMSFTDQEDTSCSSEVYFDRASVTALLPPHPKNGPTLOERKSKYKALITLYLIV 60

Qy 61 FVVLVPIIGIYAAQLKMETKCTVGSVNAD-ISPSPGKNGSGSDENKFRFAVNERMSN 119

61 FAVLPITAIIMAAQLKMKMCKCTGSIANSVSSLLGRGNDSEBEVAFREVMHEHSK 120

Qy 120 MESRIQYISDNEANLLDAKNFQNSITTDQRENDVLFQNLSSLSIOEHENIIGISKSL 179

121 MEKRIQYISDNEANLLDAKNFQNSITTDQRENDVLFQNLSSLSIOEHENIIGISKSL 180

Qy 180 VGLNTTVLDLPISITLNGRVOENAFKQOEKREKLEERLYNNAASAIKSIDEKQVYLEOEI 239

181 ISLNTTLLDLHLVETLVNFKFQENTLKQGEETSKLERVHNASAEIMSKKEQVHLEOEI 240

Qy 240 KGEMLNNITNDLRLKQWHSQTLRNITLIG 272

241 KREAVLNITNDLRLKQWHSQTLRNITLIG 273

RESULT 7

146862

macrophage scavenger receptor, splice form I - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C>Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 09-Jul-2004

C:Accession: I46862

R:Bickel, P.E.; Freeman, M.W.

J. Clin. Invest. 90, 1450-1457, 1992

A:Title: Rabbit aortic smooth muscle cells express inducible macrophage scavenger recept

A:Reference number: I46862; PMID:93016877; PMID:1401078

A:Accession: I46862

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-454 <BIC>

A:Cross-references: UNIPROT:Q05585; UNIPARC:UPI000012F667; GB:U11693; NID:G165508; PIN:

C:Superfamily: macrophage scavenger receptor; scavenger receptor cysteine-rich domain ho

C:Keywords: alternative splicing

F:350-453/Domain: scavenger receptor cysteine-rich domain homology <SRC>

Query Match 48.0%; Score 987.5; DB 2; Length 454;

Best Local Similarity 68.9%; Pred. No. 1.7e-54;

Matches 188; Conservative 44; Mismatches 40; Indels 1; Gaps 1;

Qy 1 MAQMDPFDQEDTSCSSEVYFDRASVTALLPPHPKNGPTLOERKSKYKALITLYLIV 60

1 MAQMSFTDQEDTSCSSEVYFDRASVTALLPPHPKNGPTLOERKSKYKALITLYLIV 60

Qy 61 FVVLVPIIGIYAAQLKMETKCTVGSVNAD-ISPSPGKNGSGSDENKFRFAVNERMSN 119

61 FAVLPITAIIMAAQLKMKMCKCTGSIANSVSSLLGRGNDSEBEVAFREVMHEHSK 120

Qy 120 MESRIQYISDNEANLLDAKNFQNSITTDQRENDVLFQNLSSLSIOEHENIIGISKSL 179

121 MEKRIQYISDNEANLLDAKNFQNSITTDQRENDVLFQNLSSLSIOEHENIIGISKSL 180

Qy 180 VGLNTTVLDLPISITLNGRVOENAFKQOEKREKLEERLYNNAASAIKSIDEKQVYLEOEI 239

181 ISLNTTLLDLHLVETLVNFKFQENTLKQGEETSKLERVHNASAEIMSKKEQVHLEOEI 240

Qy 240 KGEMLNNITNDLRLKQWHSQTLRNITLIG 272

241 KREAVLNITNDLRLKQWHSQTLRNITLIG 273

Db 241 KREAVLNITNDLRLKQWHSQTLRNITLIG 273

RESULT 8

173338

macrophage scavenger receptor, splice form II - mouse

C:Species: Mus musculus (house mouse)

C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 22-Oct-1999

C:Accession: I73338; B38260

R:Ashkenas, D.; Penman, M.; Vassile, E.; Acton, S.; Freeman, M.W.; Krieger, M.

J. Lipid Res. 34, 983-1000, 1993

A:Title: Structures and high and low affinity ligand binding properties of murine type I

A/Contents: sequences of tryptic peptides
A/Accession: A92092
A/Molecule type: protein
A/Residues: 25-57, T, 59-76, E, 78-152 <DE12>
A/Cross-references: UNIPARC:UPI00000373A3
R/Livnah, O., Sussman, J.
A/Reference number: A51448; PDB:2AVI
A/Contents: annotation; X-ray crystallography, 3.0 angstroms, with biotin, residues 27-57
R/Livnah, O., Beyer, E.A., Wilchek, M., Sussman, J.L.
Proc. Natl. Acad. Sci. U.S.A. 90, 5076-5080, 1993
A/Title: Three-dimensional structures of avidin and the avidin-biotin complex.
A/Reference number: A47554; PMID:93281699; PMID:8506353
A/Contents: annotation; X-ray crystallography, 3.0 angstroms
R/Pugliese, L., Coda, A., Malcovati, M., Bolognesi, M.
Submitted to the Brookhaven Protein Data Bank, March 1993
A/Reference number: A51622; PDB:1AVD
A/Contents: annotation; X-ray crystallography, 2.7 angstroms, with biotin, residues 27-57
R/Pugliese, L., Coda, A., Malcovati, M., Bolognesi, M.
Submitted to the Brookhaven Protein Data Bank, March 1993
A/Reference number: A51623; PDB:1AVR
A/Contents: annotation; X-ray crystallography, 2.8 angstroms, without biotin, residues 27-57
R/Pugliese, L., Coda, A., Malcovati, M., Bolognesi, M.
J. Mol. Biol. 231, 698-710, 1993
A/Title: Three-dimensional structure of the tetragonal crystal form of egg-white avidin
A/Reference number: A54974; PMID:93294833; PMID:8515446
A/Contents: annotation; X-ray crystallography, 2.7 angstroms
C/Genetics: CH1
A/Introns: 27/3, 98/1, 138/2
C/Superfamily: avidin
C/Keywords: glycoprotein
F/1-24/Domain: signal sequence #status predicted <Sig>
F/25-150/Product: avidin #status experimental <Mat>
F/28-105/Diulfide bonds: #status experimental
F/41/Binding site: carboxydrate (Asn) (covalent) #status experimental

Query Match 32.9%; Score 678; DB 1; Length 152;
Best Local Similarity 100.0%; Pred. No. 9.6e-36;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 273 ARKCSLTGKMTNDLSNMITGAVNSRGFTGYITAVTATSNIEKESPLHGQTINKRT 332
Db 25 ARKCSLTGKMTNDLSNMITGAVNSRGFTGYITAVTATSNIEKESPLHGQTINKRT 84

Qy 333 OPTFGFTVNMKSESSTVFTGQCFIDRNGKEVLKTMMLRSSVNDIGDMKATRVGINF 392
Db 85 OPTFGFTVNMKSESSTVFTGQCFIDRNGKEVLKTMMLRSSVNDIGDMKATRVGINF 144

Qy 393 TRLRTQKE 400
Db 145 TRLRTQKE 152

RESULT 11
S42204
Avidin-related protein 4/5 precursor - chicken
C/Species: Gallus gallus (chicken)
C/Date: 13-Jan-1995 #sequence revision 13-Jan-1995 #text_change 09-Jul-2004
C/Accession: S42204; S42205
R/Keinaenen, R.A.; Wallen, M.J.; Kristo, P.A.; Laukkanen, M.O.; Toimela, T.A.; Helenius, E.
Eur. J. Biochem. 220, 615-621, 1994
A/Title: Molecular cloning and nucleotide sequence of chicken avidin-related genes 1-5.
A/Reference number: S42201; PMID:94170814; PMID:8125122
A/Accession: S42204
A/Molecule type: DNA
A/Residues: 1-150 <KE1>
A/Cross-references: UNIPROT:P56734; UNIPARC:UPI0000126678; EMBL:Z22883; NID:G311811
A/Experimental source: strain white leghorn; tissue oviduct
A/Genetics: CH1
A/Accession: S42205
A/Molecule type: DNA
A/Residues: 1-150 <KEW>
A/Cross-references: UNIPARC:UPI0000126678; EMBL:Z22882; NID:G311812

A/Experimental source: strain white leghorn; tissue oviduct
A/Genetics: CH2
C/Genetics: <CH1>
A/Gene: avr4
A/Introns: 27/3, 96/1, 136/2
C/Genetics: <CH2>
A/Gene: avr5
A/Introns: 27/3, 96/1, 136/2
C/Superfamily: avidin
F/1-24/Domain: signal sequence #status predicted <Sig>
F/25-150/Product: avidin-related protein 4/5 #status predicted <Mat>
F/28-105/Diulfide bonds: #status predicted

Query Match 23.8%; Score 491; DB 2; Length 150;
Best Local Similarity 76.6%; Pred. No. 4.7e-24;
Matches 98; Conservative 7; Mismatches 21; Indels 2; Gaps 1;

Qy 273 ARKCSLTGKMTNDLSNMITGAVNSRGFTGYITAVTATSNIEKESPLHGQTINKRT 332
Db 25 ARKCSLTGKMTNDLSNMITGAVNSRGFTGYITAVADNPNTILSPLLGIQH--KRAS 82

Qy 333 OPTFGFTVNMKSESSTVFTGQCFIDRNGKEVLKTMMLRSSVNDIGDMKATRVGINF 392
Db 83 OPTFGFTVNMKSESSTVFTGQCFIDRNGKEVLKTMMLRSSVNDISYDMKATRVGINF 142

Qy 393 TRLRTQKE 400
Db 143 TRLRTQKE 150

RESULT 12
S42203
Avidin-related protein 3 precursor - chicken
N/Alternate names: avr3 protein
C/Species: Gallus gallus (chicken)
C/Date: 13-Jan-1995 #sequence revision 13-Jan-1995 #text_change 09-Jul-2004
C/Accession: S42203; S39800
R/Keinaenen, R.A.; Wallen, M.J.; Kristo, P.A.; Laukkanen, M.O.; Toimela, T.A.; Helenius, E.
Eur. J. Biochem. 220, 615-621, 1994
A/Title: Molecular cloning and nucleotide sequence of chicken avidin-related genes 1-5.
A/Reference number: S42201; PMID:94170814; PMID:8125122
A/Accession: S42203
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-150 <KE1>
A/Cross-references: UNIPROT:P56733; UNIPARC:UPI0000126677; EMBL:Z21612; NID:G65432
R/Kunna, T.A.; Wallen, M.J.; Kulomaa, M.S.
Biochim. Biophys. Acta 1216, 441-445, 1993
F/1-24/Domain: signal sequence #status predicted <Sig>
F/25-150/Product: induction of chicken avidin and related mRNAs after bacterial infection.
A/Reference number: S39799; PMID:94092737; PMID:8268225
A/Accession: S39800
A/Status: preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 71-150 <KUN>
A/Cross-references: UNIPARC:UPI0000178FD; EMBL:Z21536; NID:G65429
C/Genetics: CH1
A/Gene: avr3
A/Introns: 27/3, 96/1, 136/2
C/Superfamily: avidin
F/1-24/Domain: signal sequence #status predicted <Sig>
F/25-150/Product: signal sequence #status predicted <Mat>
F/28-105/Diulfide bonds: #status predicted

Query Match 22.4%; Score 461; DB 2; Length 150;
Best Local Similarity 71.1%; Pred. No. 3.6e-22;
Matches 91; Conservative 10; Mismatches 25; Indels 2; Gaps 1;

Qy 273 ARKCSLTGKMTNDLSNMITGAVNSRGFTGYITAVTATSNIEKESPLHGQTINKRT 332
Db 25 ARKCSLTGKMTNDLSNMITGAVNSRGFTGYITAVADNPNTILSPLLGIQH--KRAC 82

Qy 333 OPTFGFTVNMKSESSTVFTGQCFIDRNGKEVLKTMMLRSSVNDIGDMKATRVGINF 392
Db 143 TRLRTQKE 150

F/218-249/Domains: EGF homology <EG03>
 F/256-287/Domains: EGF homology <EG04>
 F/294-325/Domains: EGF homology <EG05>
 F/332-363/Domains: EGF homology <EG06>
 F/370-401/Domains: EGF homology <EG07>
 F/408-439/Domains: EGF homology <EG08>
 F/446-477/Domains: EGF homology <EG09>
 F/484-515/Domains: EGF homology <EG10>
 F/522-553/Domains: EGF homology <EG11>
 F/560-591/Domains: EGF homology <EG12>
 F/598-629/Domains: EGF homology <EG13>
 F/636-667/Domains: EGF homology <EG14>
 F/674-705/Domains: EGF homology <EG15>
 F/712-743/Domains: EGF homology <EG16>
 F/750-781/Domains: EGF homology <EG17>
 F/788-819/Domains: EGF homology <EG18>
 F/826-857/Domains: EGF homology <EG19>
 F/864-895/Domains: EGF homology <EG20>
 F/902-933/Domains: EGF homology <EG21>
 F/936-1064/Region: avidin-like
 F/23-34,28-43,45-54,62-88,180-191,185-200,202-211,218-229,223-238,240-249,256-267,261-27
 5,451-466,468-477,484-495/Duplicate bonds: #status predicted
 F/489-504,506-515,522-533,527-542,544-553,560-571,565-580,582-591,598-609,603-618,620-62
 08,810-819,826-837,831-846,848-857,864-875,869-884,886-895,902-913,907-922,924-933/Duplicate

Query Match 6.8%; Score 140; DB 2; Length 1064;

Best Local Similarity 33.6%; Pred.No.0.56; 51; Indels 16; Gaps 4;

Matches 42; Conservative 16; Mismatches 51;

QY 276 CSLTGKWTNDLGSNMITIGAVNSRGEFTGYITAVTATSNIEKSPHAGTQNTI-----N 329
 DB 939 CDLEGMWNECDQYTI-TKISTGMMLGDYMT-----YNERALGYAAPTVVVGYSN 989
 QY 330 KKTQPTFGFTVMKPSSESTTVFTGQCIFDRNGKEVILKTMWLLRSSVNDIGDDMKATRVGI 389
 DB 990 NYDPSPFGFTVVRDNGQSTTSWTCQCHL-CDGESEVLYTTWINTNMVSTCQDIKSNMVQ 1048
 QY 390 NIFTR 394
 DB 1049 DKWTR 1053

Search completed: February 16, 2006, 17:05:47
 Job time : 42 secs

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Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 16, 2006, 16:58:02 ; Search time 231 Seconds

(without alignments)
1221.694 Million cell updates/sec

Title: US-10-618-570-2

Perfect score: 2059
Sequence: 1 MAQMDPFDQDQEDTDSCTES.....DKATRVGINIFRLRQKE 400

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80.*

1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1381	67.1	453	1 MSRE_BOVIN	P21758 boe tauru
2	1042.5	50.6	388	2 O60505_HUMAN	O60505 homo sapie
3	1042.5	50.6	451	1 MSRE_HUMAN	P21757 homo sapie
4	987.5	48.0	454	1 MSRE_RABIT	Q05585 oryctolagus
5	830	40.3	354	2 O8CED7_MOUSE	O8ced7 mus musculu
6	801	38.9	458	1 MSRE_MOUSE	P31204 mus musculu
7	675	32.8	152	1 AVID_CHICK	P02701 gallus galli
8	664	32.8	152	2 O98SH4_CHICK	O98sh4 gallus galli
9	491	32.8	150	1 AVR4_CHICK	P56734 gallus galli
10	483.5	23.5	122	2 O8AY76_MEUGA	O8ay76 meileagris g
11	461	22.4	150	1 AVR3_CHICK	P56733 gallus galli
12	461	22.4	150	1 AVR7_CHICK	P56736 gallus galli
13	452	22.0	150	1 AVR1_CHICK	O13153 gallus galli
14	451	21.9	150	1 AVR6_CHICK	P56735 gallus galli
15	436	21.2	150	1 AVR2_CHICK	P56732 gallus galli
16	233	11.3	95	2 P70111_MESAU	P70111 mesocricetu
17	219	10.6	499	2 O5RFW0_BRABE	O5rfw0 brachydanto
18	204	9.9	400	2 O8A427_HUMAN	O8a427 homo sapie
19	204	9.9	495	2 O6ZMJ2_HUMAN	O6zmj2 homo sapie
20	199.5	9.7	374	2 O9CUC3_MOUSE	O9cuc3 mus musculu
21	195.5	9.5	491	2 O81WDC_MOUSE	O81wdc mus musculu
22	194.5	9.4	387	2 O8BZ22_MOUSE	O8bz22 mus musculu
23	194.5	9.4	491	2 O8K299_MOUSE	O8k299 mus musculu
24	173.5	8.4	410	2 O4RF52_TENG	O4rf52 tetracodon n
25	164.5	8.0	357	2 O7Z4A1_HUMAN	O7z4a1 homo sapie
26	163.5	7.9	280	2 O9D4G8_MOUSE	O9d4g8 mus musculu
27	144	7.0	283	2 O8R330_MOUSE	O8r330 mus musculu
28	144	7.0	1190	2 O519A0_ENTHI	O519a0 entameoba h
29	141.5	6.9	778	2 O96WJ2_KULULA	O96wj2 kluyveromyc
30	141	6.8	980	2 O73ML2_TREDE	O73ml2 treponema d
31	140	6.8	1064	1 FBPI_STRPV	P10079 strongyloce

32	139.5	6.8	183	1 SAV2_STRVL	O53533 streptomyce
33	138.5	6.7	183	1 SAV1_STRVL	O53532 streptomyce
34	138.5	6.7	183	1 SAV_STRVL	P22629 streptomyce
35	138.5	6.7	947	2 O61F09_PLAF7	O61f09 plasmodium
36	136	6.6	529	2 O25058_HELD	O25058 heliocidari
37	135.5	6.6	9439	2 O8CP76_STAE	O8cp76 staphylococ
38	135.5	6.6	10203	2 O5HPA2_STAE	O5hpa2 staphylococ
39	133.5	6.5	715	2 O51542_BORBU	O51542 borrelia bu
40	133.5	6.4	466	2 O8R3P2_MOUSE	O8r3p2 mus musculu
41	132.5	6.4	543	2 O8BHK4_MOUSE	O8bmk4 mus musculu
42	132.5	6.4	570	2 O97FD7_CIOAB	O97fd7 clostridium
43	132.5	6.4	1163	1 SBCC_CIOAB	O97fki clostridium
44	132	6.4	657	2 O4S759_TENG	O4s759 tetracodon n
45	132	6.4	1461	2 O6KHx4_MYCWO	O6kx4 mycoplasma

ALIGNMENTS

RESULT 1

MSRE_BOVIN

ID MSRE_BOVIN STANDARD: PRT: 453 AA.

AC P21758;

DT 01-MAY-1991 (Rel. 18, Created)

DT 01-MAY-1991 (Rel. 18, Last sequence update)

DT 10-MAY-2005 (Rel. 47, Last annotation update)

DE Macrophage scavenger receptor types I and II (Macrophage acetylated

LDL receptor I and II).

GN Name=MSRL;

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;

OC Pecora; Bovidae; Bovinae; Bos.

OC NCBI_TaxId=9913;

NP NUCLEOTIDE SEQUENCE, AND PARTIAL PROTEIN SEQUENCE.

RC TISSUE=Lung;

RX MEDLINE=90136965; PubMed=2300204; DOI=10.1038/34351a0;

RA Kodama T., Freeman M., Rohrer L., Zabrecky J., Matcudaira P.,

RA Krieger M.;

RT "Type I macrophage scavenger receptor contains alpha-helical and

RT collagen-like coiled coils.";

RL Nature 343:531-535(1990).

[2]

NP NUCLEOTIDE SEQUENCE (ISOFORM SHORT).

RC TISSUE=Lung;

RX MEDLINE=90136973; PubMed=2300208; DOI=10.1038/343570a0;

RA Rohrer L., Freeman M., Kodama T., Penman M., Krieger M.;

RA "Coiled-coil fibrous domains mediate ligand binding by macrophage

RT scavenger receptor type II.";

RL Nature 343:570-572(1990).

-1- FUNCTION: Membrane glycoproteins implicated in the pathologic

deposition of cholesterol in arterial walls during atherogenesis.

Two types of receptor subunits exist. These receptors mediate the

endocytosis of a diverse group of macromolecules, including

modified low density lipoproteins (LDL).

-1- SUBUNIT: Homotrimer.

-1- SUBCELLULAR LOCATION: Type II membrane protein.

-1- ALTERNATIVE PRODUCTS:

Event=Alternative splicing; Named isoforms=2;

Name=I;

Name=II;

IsoId=P21758-1; Sequence=Displayed;

IsoId=P21758-2; Sequence=VSP_006227, VSP_006228;

-1- SIMILARITY: Contains 1 collagen-like domain.

-1- SIMILARITY: Contains 1 SRCR domain.

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removed.

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DR EMBL; X51689; CAA35987.1; -; mRNA.  
DR EMBL; X54183; CAA38108.1; -; mRNA.  
DR PIR; S08276; S08276.  
DR PIR; S08278; S08278.  
DR InterPro; IPR008161; C1g_helix.  
DR InterPro; IPR008160; Collagen.  
DR InterPro; IPR003543; Macscav_receptor.  
DR InterPro; IPR001190; Srcr_receptor.  
DR PANTHER; PTHR19311.SF5; Macscav_receptor; 1.  
DR Pfam; PF01391; Collagen; 1.  
DR Pfam; PF03523; Macscav_rec; 1.  
DR Pfam; PF00530; SRCR; 1.  
DR PRINTS; PR01408; MACSCAVRCPTR.  
DR PRINTS; PR00258; SPERACTRCPTR.  
DR PRODOM; PD000007; C1g_helix; 1.  
DR SMART; SM00202; SR; 1.  
DR PROSITE; PS00420; SRCR_1; 1.  
DR PROSITE; PS50287; SRCR_2; 1.  
DR Alternative splicing; Collcd coll; Collagen;  
KW Direct protein sequencing; Endocytosis; Glycoprotein; LDL; Receptor;  
KW Signal-anchor; Transmembrane.  
FT TOPO_DOM 1 50 Cytoplasmic (potential).  
FT TRANSMEM 51 76 Signal-anchor for type II membrane  
FT FT protein (potential).  
FT TOPO_DOM 77 453 Extracellular (potential).  
FT DOMAIN 272 343 Collagen-like.  
FT REGION 352 452 SRCR.  
FT REGION 77 108 Spacer (probable).  
FT COLLED 194 255 Potential.  
FT CARBOHYD 82 82 N-linked (GlcNAc... ) (potential).  
FT CARBOHYD 101 101 N-linked (GlcNAc... ) (potential).  
FT CARBOHYD 142 142 N-linked (GlcNAc... ) (potential).  
FT CARBOHYD 183 183 N-linked (GlcNAc... ) (potential).  
FT CARBOHYD 220 220 N-linked (GlcNAc... ) (potential).  
FT CARBOHYD 248 248 N-linked (GlcNAc... ) (potential).  
FT CARBOHYD 266 266 N-linked (GlcNAc... ) (potential).  
FT DISULFID 377 441 By similarity.  
FT DISULFID 390 451 By similarity.  
FT DISULFID 421 431 By similarity.  
FT VASAPLIC 348 349 OS -> PG (in isoform II).  
FT VASAPLIC 350 453 /FTId=VSP_006227.  
FT VASAPLIC 350 453 Missing (in isoform II).  
FT VASAPLIC 350 453 /FTId=VSP_006228.  
SQ SEQUENCE 453 AA; 50057 MW; 77A0FEFE48B00A21 CRC64;  
Query Match 67.1%; Score 1381; DB 1; Length 453;  
Best Local Similarity 100.0%; Pred. No. 2.2e-75;  
Matches 272; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
AC O60505;  
DT 01-AUG-1998 (TRENBLREL. 07, Created)  
DT 01-AUG-1998 (TRENBLREL. 07, Last sequence update)  
DT 01-MAR-2004 (TRENBLREL. 26, Last annotation update)  
DE Macrophage scavenger receptor type III.  
GN Name=SR-A;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;  
OC Homo  
OX NCBI_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=98208366; PubMed=9548586;  
RA Gough P.J., Greaves D.R., Gordon S.;  
RT "A naturally occurring isoform of the human macrophage scavenger  
RT receptor (SR-A) gene generated by alternative splicing blocks modified  
RT LDL uptake."  
RT J. Lipid Res. 39:531-543(1998).  
RL EMBL; AF037351; AAC09251.1; -; mRNA.  
DR HSSP; Q08380; 1BY2.  
DR Ensembl; ENSG00000038945; Homo sapiens.  
DR GO; GO:0005737; C:cytoplasm; IEA.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR GO; GO:0005044; F:scavenger receptor activity; IEA.  
DR GO; GO:0006817; P:phosphate transport; IEA.  
DR GO; GO:0006898; P:receptor mediated endocytosis; IEA.  
DR InterPro; IPR008161; C1g_helix.  
DR InterPro; IPR008160; Collagen.  
DR InterPro; IPR003543; Macscav_receptor.  
DR InterPro; IPR001190; Srcr_receptor.  
DR Pfam; PF01391; Collagen; 1.  
DR Pfam; PF03523; Macscav_rec; 1.  
DR Pfam; PF00530; SRCR; 1.  
DR PRINTS; PR01408; MACSCAVRCPTR.  
DR PRINTS; PR00258; SPERACTRCPTR.  
DR PRODOM; PD000007; C1g_helix; 1.  
DR SMART; SM00202; SR; 1.  
DR PROSITE; PS50287; SRCR_2; 1.  
KW Collagen; Receptor.  
SQ SEQUENCE 388 AA; 42942 MW; D6A20BC57BFB64 CRC64;  
Query Match 50.6%; Score 1042.5; DB 2; Length 388;  
Best Local Similarity 72.2%; Pred. No. 5.3e-55;  
Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;
```

```
QY 1 MAQMDPFDQOEDTDSCTESVYKFDARSTVALLPPHPKNGPTLQERMKSYKTALITLYLIV 60  
DB 1 MAQMDPFDQOEDTDSCTESVYKFDARSTVALLPPHPKNGPTLQERMKSYKTALITLYLIV 60  
QY 61 FVVLVPIIIGVAAQLLKMETKNCVGSVNA-DISPEBGKNGSEDEMRPREAVMERNSM 120  
DB 61 FVVLVPIIIGVAAQLLKMETKNCVGSVNA-DISPEBGKNGSEDEMRPREAVMERNSM 120  
QY 121 ESRIOYLSNENANLLDAKNFONFSITTDQRFNDVLFQNLSSLSIOEHENIIGDISKSLV 180  
DB 121 ESRIOYLSNENANLLDAKNFONFSITTDQRFNDVLFQNLSSLSIOEHENIIGDISKSLV 180  
QY 181 GLNTTVLDLQFSIETLNGRVOENAFKQOEEMRKLEERIYNASAEIKSLDEKQVYLEOEIK 240  
DB 181 GLNTTVLDLQFSIETLNGRVOENAFKQOEEMRKLEERIYNASAEIKSLDEKQVYLEOEIK 240  
QY 241 GEMKLNNTTNDRLKQWEHSQTLKNITLLQG 272  
DB 241 GEMKLNNTTNDRLKQWEHSQTLKNITLLQG 272
```

RESULT 2
O60505_HUMAN
ID O60505_HUMAN PRELIMINARY; PRT; 388 AA.

```
QY 1 MAQMDPFDQOEDTDSCTESVYKFDARSTVALLPPHPKNGPTLQERMKSYKTALITLYLIV 60  
DB 1 MEQMDHFHQOEDTDSCTESVYKFDARSTVALLPPHPKNGPTLQERMKSYKTALITLYLIV 60  
QY 61 FVVLVPIIIGVAAQLLKMETKNCVGSVNA-DISPEBGKNGSEDEMRPREAVMERNSM 119  
DB 61 FVVLVPIIIGVAAQLLKMETKNCVGSVNA-DISPEBGKNGSEDEMRPREAVMERNSM 120  
QY 120 MESRIOYLSNENANLLDAKNFONFSITTDQRFNDVLFQNLSSLSIOEHENIIGDISKSL 179  
DB 120 MESRIOYLSNENANLLDAKNFONFSITTDQRFNDVLFQNLSSLSIOEHENIIGDISKSL 180  
QY 180 GLNTTVLDLQFSIETLNGRVOENAFKQOEEMRKLEERIYNASAEIKSLDEKQVYLEOEI 239  
DB 180 GLNTTVLDLQFSIETLNGRVOENAFKQOEEMRKLEERIYNASAEIKSLDEKQVYLEOEI 240  
QY 240 KGEKLNNTTNDRLKQWEHSQTLKNITLLQG 272  
DB 240 KGEKLNNTTNDRLKQWEHSQTLKNITLLQG 273
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RESULT 3
MSRE_HUMAN
ID MSRE_HUMAN STANDARD; PRT; 451 AA.
AC P21757; P21759;
DT 01-MAY-1991 (Rel. 18, Created)

DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Macrophage scavenger receptor types I and II (Macrophage acetylated
DS LDL receptor I and II) (CD204 antigen).
GN Name=MSR1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
CC NCBI_TaxID=9606;
CC [1]
RN NUCLEOTIDE SEQUENCE (ISOFORMS I AND II).
RP MEDLINE=91067661; PubMed=2251254;
RX Matsumoto A., Naito M., Itakura H., Ikemoto S., Asaoka H.,
RA Hayakawa I., Kanamori H., Aburatani H., Takaku F., Suzuki H.,
RA Kobari T., Miyai T., Takahashi K., Cohen E.H., Wydro R., Housman D.E.,
RT Kodama T.;
RT "Human macrophage scavenger receptors: primary structure, expression,
RT and localization in atherosclerotic lesions";
RL Proc. Natl. Acad. Sci. U.S.A. 87:9133-9137 (1990).
[2]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM I).
RP TISSUE=Testis;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Bluetow K.H., Schaefel C.F., Bat N.K.,
RA Hopkins R.F., Jordan K.C., Moore T., Max S.I., Wang Y., Heide F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stepien M., Soares M.B., Bonaldi M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Tomshyuk S., Cantarel P., Prange S.J.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Holton E., Ketteman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Bridges A.C., Grimmwood J.C., Schmütz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzyzinski M.I., Skalska U., Smallus D.E.,
RA Scheraga A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[3]
RN NUCLEOTIDE SEQUENCE OF 155-272.
RX PubMed=8093617;
RA Ent M., Asaoka H., Matsumoto A., Itakura H., Kurihara Y., Wada Y.,
RA Kanamori H., Yaaki Y., Takahashi B., Legeat M.;
RT "Structure, organization, and chromosomal mapping of the human
RT macrophage scavenger receptor gene.";
RL J. Biol. Chem. 268:2120-2125 (1993).
[4]
RN SRCR DOMAIN DISULFIDE BONDS.
RP MEDLINE=85900117; PubMed=85900177; DOI=10.1074/jbc.271.43.26524;
RX Resnick D., Chetail J.E., Schwartz K., Slayer H., Krieger M.;
RT "Structures of class A macrophage scavenger receptors. Electron
RT microscopic study of flexible, multidomain, fibrous proteins and
RT determination of the disulfide bond pattern of the scavenger receptor
RT cytosine-rich domain.";
RL J. Biol. Chem. 271:26524-26530 (1996).
[5]
RN SPICE ISOFORM(S) THAT ARE POTENTIAL NMD TARGET(S).
RX PubMed=14759258; DOI=10.1186/gb-2004-5-2-r8;
RA Hillman R.T., Green R.E., Brenner S.E.;
RT "An unappreciated role for RNA surveillance.";
RA Genome Biol. 5:RBSBACH008.1-RBSBACH008.16(2004).
CC *-1- FUNCTION: Membrane glycoproteins implicated in the pathologic
CC deposition of cholesterol in arterial walls during atherogenesis.
CC Two types of receptor subunits exist. These receptors mediate the
CC endocytosis of a diverse group of macromolecules, including
CC modified low density lipoproteins (LDL).
CC *-1- SUBUNIT: Homotrimer.

CC	-I- SUBCELLULAR LOCATION: Type II membrane protein.
CC	-I- ALTERNATIVE PRODUCTS:
CC	Event=Alternative splicing; Named isoforms=2;
CC	Name=I;
CC	Id=PI21757-1; Sequence=Displayed;
CC	Name=II;
CC	Id=PI21757-2; Sequence=VSP_006229, VSP_006230;
CC	Note=May be produced at very low levels due to a premature stop
CC	codon in the mRNA, leading to nonsense-mediated mRNA decay;
CC	-I- SIMILARITY: Contains 1 collagen-like domain.
CC	-I- SIMILARITY: Contains 1 SRCR domain.
CC	This Swiss-prot entry is copyright. It is produced through a collaboration
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC	the European Bioinformatics Institute. There are no restrictions on its
CC	use as long as its content is in no way modified and this statement is not
CC	removed.
CC	-----
DR	EMBL; D90187; BAA14208.1; -; mRNA.
DR	EMBL; D90188; BAA14209.1; -; mRNA.
DR	EMBL; BC063878; AAH63878.1; -; mRNA.
DR	EMBL; D13263; -; NOT_ANNOTATED_CDS; Genomic_DNA.
DR	PIR; A38415; A38415.
DR	PIR; B38415; B38415.
DR	Ensembl; ENSG00000038945; Homo sapiens.
DR	HGN; HGNC; 7376; NSRI.
DR	MIM; 153622; -.
DR	GO; GO:0005887; C:integral to plasma membrane; TAS.
DR	GO; GO:0005044; F:scavenger receptor activity; TAS.
DR	GO; GO:0006898; P:receptor mediated endocytosis; TAS.
DR	InterPro; IPR008161; Clg_helix.
DR	InterPro; IPR008160; Collagen.
DR	InterPro; IPR003543; Macscav_receptor.
DR	InterPro; IPR001190; Srcr_receptor.
DR	PANTHER; PTHR19331.SF5; Macscav_receptor; 1.
DR	PFam; PF01391; Collagen; 1.
DR	PFam; PR03523; Macscav_rec; 1.
DR	PFam; PF00530; SRCR; 1.
DR	PRINTS; PRO1408; MACSCAVRCPTR.
DR	PRINTS; PRO0258; SPERACTRCPTR.
DR	Prodom; PD000007; Clg_helix; 1.
DR	SMART; SM00202; SR; 1.
DR	PROSITE; PS00420; SRCR_1; 1.
DR	PROSITE; PS50287; SRCR_2; 1.
KW	Alternative splicing; Antigen; Coiled coil; Collagen; Endocytosis;
KM	Glycoprotein; LDL; Receptor; Signal-anchor; Transmembrane.
FT	TOPO_DOM 1 50
FT	TRANSMEM 51 76
FT	TOPO_DOM 77 451
FT	DOMAIN 273 341
FT	DOMAIN 350 450
FT	REGION 77 109
FT	COILED 171 255
FT	CARBOHYD 82 82
FT	CARBOHYD 102 102
FT	CARBOHYD 143 143
FT	CARBOHYD 184 184
FT	CARBOHYD 221 221
FT	CARBOHYD 249 249
FT	CARBOHYD 267 267
FT	DISULFID 375 439
FT	DISULFID 388 449
FT	DISULFID 419 429
FT	VARSPLIC 345 358
FT	TPTKTVLVGGSGP -> RPVLTLDIRAGPS (in
FT	isoform II).
FT	/FTid=VSP_006229.
FT	Missing (in isoform II).
FT	/FTid=VSP_006230.
FT	VARSPLIC 359 451
FT	SEQUENCE 451 AA; 49762 MW; 915CQ3B653BA1 CRC64;
SO	Query Match 50.6%; Score 1042.5; DB 1; Length 451;
	Best Local Similarity 72.2%; Pred. No. 6; e=-55;

Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;

QY 1 MAQNDPDPQOEDDCTESYKFPDARSVTALLPBPKNQPTLQERMSKYKATLITLYIV 60
 DB 1 MEQNDHFNQOEDDCTESYKFPDARSVTALLPBPKNQPTLQERMSKYKATLITLYIV 60
 QY 61 FVULVPIIGIYAAQOLKMKETKNCVGSVNA-DISPSPGKNGSEDEMRPREAWERNMN 119
 DB 61 FAVLIPILIGIYAAQOLKMKETKNCVGSVSNANDITQSLTGKNGDSEERKPFQEFMEHNSN 120
 QY 120 MESRIQVLSDEANLIDAKNFQNSITTDQRFNVLFQNLISLSIOGHENITGDISKSL 179
 DB 121 MEKRIQHLIDMEANLIDMEHNFQNSITTDQRFNVLFQNLISLSIOGHENITGDISKSL 180
 QY 180 VGLNTTVLDLQFSTIETLNGRVOENAFKQOEBMRKLEERINYASAEIKSLDEKQVYLEOEI 239
 DB 181 ISLNTTLLDLHLVETLNVKQEWTLKGQEBISKLKEVRHNASABIMKKEQVHLEOEI 240
 QY 240 KGEKMLANNITNDRLKDMWHSQTLRNITLLQG 272
 DB 241 KREVYLVANNITNDRLKDMWHSQTLRNITLLQG 273

RESULT 4
 MSRE_RABIT STANDARD; PRT; 454 AA.
 ID MSRE_RABIT 005585;
 AC 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Macrophage scavenger receptor types I and II (Macrophage acetylated LDL receptor I and II).
 GN Name=MSR1;
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae; Oryctolagus.
 OC NCBI_TaxID=9986;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=93016877; PubMed=1401078;
 RA Bickel P.E., Freeman M.W.;
 RT "Rabbit aortic smooth muscle cells express inducible macrophage scavenger receptor messenger RNA that is absent from endothelial cells";
 RL J. Clin. Invest. 90:1450-1457(1992).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=93131972; PubMed=8380589;
 RA Doi T., Wada Y., Kodama T., Higashi K.I., Kurihara Y., Miyazaki T., Nakamura H., Ueugli S., Imanishi T., Kawabe Y., Itakura H., Yazaki Y., Matsunoto A.;
 RT "Charged collagen structure mediates the recognition of negatively charged macromolecules by macrophage scavenger receptors";
 RL J. Biol. Chem. 268:2126-2133(1993).
 CC -1- FUNCTION: Membrane glycoproteins implicated in the pathologic deposition of cholesterol in arterial walls during atherosclerosis. Two types of receptor subunits exist. These receptors mediate the endocytosis of a diverse group of macromolecules, including endocytosis of low density lipoproteins (LDL).
 CC -1- SUBUNIT: Homotrimer.
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=I;
 CC IsoId=Q05585-1; Sequence=Displayed;
 CC Name=II;
 CC IsoId=Q05585-2; Sequence=VSP_006233, VSP_006234;
 CC -1- SIMILARITY: Contains 1 collagen-like domain.
 CC -1- SIMILARITY: Contains 1 SRCR domain.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.

CC EMBL; L11693; AAA31402.1; -; mRNA.
 CC EMBL; L11692; AAA31403.1; -; mRNA.
 CC EMBL; D13381; BAA02649.1; -; mRNA.
 CC PIR; I46862; I46862.
 CC PIR; I46863; I46863.
 CC InterPro; IPR008161; C1g helix.
 CC InterPro; IPR008160; Collagen.
 CC InterPro; IPR003543; Macscav_receptor.
 CC InterPro; IPR001190; Src_receptor.
 CC PANTHER; PTHR19331:SF5; Macscav_receptor; 1.
 CC Pfam; PF01391; Collagen; 1.
 CC Pfam; PF03523; Macscav_rec; 1.
 CC Pfam; PF00530; SRCR; 1.
 CC PRINTS; PR01408; MACSCAVRCPTR.
 CC PRINTS; PR00258; SPERACTRCPTR.
 CC ProDom; PD000007; C1g helix; 1.
 CC SMART; SM00420; SR; 1.
 CC PROSITE; PS00420; SRCR_1; 1.
 CC PROSITE; PS0287; SRCR_2; 1.
 CC K0 Alternative splicing; Coiled
 KW Glycoprotein; LDL; Receptor;
 FT TOPO_DOM 1 50
 FT TRANSMEM 51 73
 FT TOPO_DOM 74 454
 FT DOMAIN 273 344
 FT DOMAIN 353 453
 FT REGION 74 109
 FT COILED 199 256
 FT CARBOHYD 82 82
 FT CARBOHYD 102 102
 FT CARBOHYD 143 143
 FT CARBOHYD 184 184
 FT CARBOHYD 221 221
 FT CARBOHYD 249 249
 FT CARBOHYD 267 267
 FT DISULFID 378 442
 FT DISULFID 391 452
 FT DISULFID 422 432
 FT VARSPLIC 348 354
 FT VARSPLIC 355 454
 FT CONFLICT 106 106
 FT SEQUENCE 454 AA; 49745 MW; 527A79692EA76429 CRC64;
 SO

Query Match 48.0%; Score 987.5; DB 1; Length 454;
 Best Local Similarity 68.9%; Pred. No. 1.4e-51;
 Matches 188; Conservative 44; Mismatches 40; Indels 1; Gaps 1;

QY 1 MAQNDPDPQOEDDCTESYKFPDARSVTALLPBPKNQPTLQERMSKYKATLITLYIV 60
 DB 1 MAQNDFTDQOEDDCTESYKFPDARSVTALLPBPKNQPTLQERMSKYKATLITLYIV 60
 QY 61 FVULVPIIGIYAAQOLKMKETKNCVGSVNA-DISPSPGKNGSEDEMRPREAWERNMN 119
 DB 61 FAVLIPILIGIYAAQOLKMKETKNCVGSVSNANDITQSLTGKNGDSEERKPFQEFMEHNSN 120
 QY 120 MESRIQVLSDEANLIDAKNFQNSITTDQRFNVLFQNLISLSIOGHENITGDISKSL 179
 DB 121 MEKRIQHLIDMEANLIDMEHNFQNSITTDQRFNVLFQNLISLSIOGHENITGDISKSL 180
 QY 180 VGLNTTVLDLQFSTIETLNGRVOENAFKQOEBMRKLEERINYASAEIKSLDEKQVYLEOEI 239
 DB 181 ISLNTTLLDLHLVETLNVKQEWTLKGQEBISKLKEVRHNASABIMKKEQVHLEOEI 240
 QY 240 KGEKMLANNITNDRLKDMWHSQTLRNITLLQG 272
 DB 241 KREVYLVANNITNDRLKDMWHSQTLRNITLLQG 273

RESULT 5
 Q8CED7_MOUSE PRELIMINARY; PRT; 354 AA.
 ID Q8CED7_MOUSE PRELIMINARY; PRT; 354 AA.
 AC Q8CED7_MOUSE PRELIMINARY; PRT; 354 AA.
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 26, Last annotation update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Mus musculus 0 day neonate skin cDNA, RIKEN full-length enriched
 DE library, clone:461424C05 product:macrophage scavenger receptor 1,
 DE full insert sequence.
 DE Name=Msr1;
 GN Mus musculus (Mouse).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OC NCBI_TaxId=10090;
 [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Skin;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning."
 RL Meth. Enzymol. 303:19-44(1999).
 [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Skin;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Aizawa K., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fletschmann W., Gaasterland T., Glasl C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nishikido I., Pesole G., Quackenbush J.,
 RA Schmitt L.M., Stambli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldi M.F.,
 RA Brownstein W.O., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Guelinich S., Hill D., Hofmann M., Hume D.A., Kamita M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima Y., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Saeki H., Sato K., Schenbach C., Seya T., Shibata K., Siorch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilmshurst L.,
 RA Wymshar-Botla A., Yoshida K., Hasegawa Y., Kawai J., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Skin;
 RA The PANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs."
 RL Nature 420:563-573(2002).
 [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Skin;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata K., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes."
 RL Genome Res. 10:1617-1630(2000).
 [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Skin;
 RX MEDLINE=20530913; PubMed=11076661; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Saeki N., Carninci P.,
 RA Kono H., Akiyama J., Nishi K., Katsunari T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
 RT "RIKEN integrated sequence analysis (RISA) system-384-Format
 RT sequencing pipeline with 384 multicapillary sequencer."
 RL Genome Res. 10:1757-1771(2000).
 [6]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Skin;
 RA Adachi J., Aizawa K., Akiyama T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hasegawa T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hironaka T.,
 RA Horii F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Kato H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK028480; BAC25973.1; -, mRNA.
 DR MGI; MGI:98257; Msr1.
 DR GO; GO:0005737; Cytoplasm; IEA.
 DR GO; GO:004872; F:receptor activity; IEA.
 DR GO; GO:0005044; F:scavenger receptor activity; IEA.
 DR GO; GO:0006817; P:phosphate transport; IEA.
 DR GO; GO:0006898; P:receptor mediated endocytosis; IEA.
 DR InterPro; IPR008161; C1g_helix.
 DR InterPro; IPR008160; C1g_helix.
 DR InterPro; IPR005453; Maccscv_receptor.
 DR InterPro; IPR002017; Spectrin.
 DR Pfam; PF01391; Collagen; 1.
 DR Pfam; PF03523; Maccscv_rec; 1.
 DR PRINTS; PR01408; MACSCVRCPR.
 DR Prodom; PD000007; C1g_helix; 1.
 KW Receptor.
 SQ SEQUENCE 354 AA, 38773 MW, 348084D2D8B644B CRC64;
 Query Match 40.3%; Score 830; DB 2; Length 354;
 Best Local Similarity 60.9%; Pred. No. 3,4e-42;
 Matches 162; Conservative 47; Mismatches 55; Indels 2; Gaps 2;
 QY 8 PPOGDTDSCTSYKVPDASVTALLPPIPKNGPTIOERKSKYKTLITLYLVFVTVPI 67
 DB 13 PHEODDADCSSESXKFDARSKMTASLPSTKNGPSLOEKKSFKALIALIYLVFVLPV 72
 QY 68 IGVAAQLLKMETKCTGVSVN-ADISPEEGKNGSEDEMFRFRAVNERMMSRSTQY 126
 DB 73 VGIVTQQLINWEMKGLVCSLNTSDTSGPKMKENTSKYEMF-TTIEHMDMERIES 131
 QY 127 LSDNEANLDAKQNFQNSITTDQRFNDVLFQNLSSLSIOEHENITIGDISKLVGNTTV 186
 DB 132 ISNSKADLIDTERFQNFMSWATDQRLNDILLQNLSSISVQEHGNSLDIAISKLSQSLNMTL 191
 QY 187 LDLOSFIEFLNGRVOENAFKQOEBMKLEERTYNSAETKSLDEKQVYIEQIKEMKLL 246
 DB 192 LDVQATTEFLNVRVESSTAKQOEDISKLEERVYKSAEVSQKAEQAHVEQSVKQEVRL 251
 QY 247 NNITNDLRKLWESHQTLKNTITLQ 272
 DB 252 NNITNDLRKLWESHQTLKNTITFIQ 277
 RESULT 6
 MSRE_MOUSE
 ID MSRE_MOUSE STANDARD; PRT; 458 AA.
 AC P30204; O923G0; Q90Z56;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)

DE Macrophage scavenger receptor types I and II (Macrophage acetylated
LDL receptor I and II) (Scavenger receptor type A) (SR-A).
GN Name=MRI; Synonyms=Scvr;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RP NUCLEOTIDE SEQUENCE (ISOFORMS I AND II).
RX MEDLINE=93359822; PubMed=8394668;
RA Ashkenas J., Penman M., Vassile E., Acton S., Freeman M.W., Krieger M.,
RT "Structures and high and low affinity ligand binding properties of
RT murine type I and type II macrophage scavenger receptors.";
RL J. Lipid Res. 34:983-1000(1993).
[2]
RP NUCLEOTIDE SEQUENCE (ISOFORM II).
RX MEDLINE=93131972; PubMed=8380589;
RA Doi T., Wada Y., Kodama T., Higashi K.I., Kurihara Y., Miyazaki T.,
RA Nakamura H., Uesugi S., Imanishi T., Kawabe Y., Itakura H., Yazaki Y.,
RA Matsumoto A.;
RT "Charged collagen structure mediates the recognition of negatively
RT charged macromolecules by macrophage scavenger receptors.";
RL J. Biol. Chem. 268:2126-2133(1993).
[3]
RP NUCLEOTIDE SEQUENCE (ISOFORM I).
RX STRAIN=C57BL/6;
RC Rateri D.L., Whitman S.C., Block A.E., Daugherty A.;
RT "Identification of a functional domain in class A scavenger receptors
RT that mediates metabolism of AcLDL.";
RL Submitted (NOV-1999) to the EMBL/Genbank/DBJ databases.
[4]
RP NUCLEOTIDE SEQUENCE (LARGE SCALE MRNA) (ISOFORM II).
RC STRAIN=NOD; TISSUE=Thymus;
RX MEDLINE=22355683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi U., Bono H., Kondo S.,
RA Nishida I., Osato N., Saito R., Suzuki H., Yamana I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gogjovski T.,
RA Balderelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schmitt L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Brad D., Brusic V., Chochia C., Corbani L.E., Cousins S.,
RA Dalla E., Dargatz T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Kanagaya A., Kurochkin I.V., Lee Y., Lemhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Petrea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Savelkin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Waranabe Y., Wells C.,
RA Wilming L.G., Wyshaw-Boris A., Yangisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carlini P., Hayatsu N.,
RA Hirozane-Tshikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imocani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,
RA Yamanishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
[5]
RP NUCLEOTIDE SEQUENCE (LARGE SCALE MRNA) (ISOFORM II).
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datschenko L., Marutian K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Uadin T.B., Toshiyuki S., Carninci P., Frange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villard D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy U., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[6]
RP NUCLEOTIDE SEQUENCE OF 349-458.
RX MEDLINE=91062370; PubMed=1978939;
RA Freeman M., Ashkenas J., Rees D.J., Kingsley D.M., Copeland N.G.,
RA Jenkins N.A., Krieger M.;
RT "An ancient, highly conserved family of cysteine-rich protein domains
RT revealed by cloning type I and type II murine macrophage scavenger
RT receptors.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:8810-8814(1990).
[7]
RP NUCLEOTIDE SEQUENCE OF 1-4.
RX MEDLINE=95395388; PubMed=7666008;
RA Aftiring R.P., Freeman M.W.;
RT "Structure of the murine macrophage scavenger receptor gene and
RT evaluation of sequences that regulate expression in the macrophage
RT cell line, P388D.";
RL J. Lipid Res. 36:1305-1314(1995).
CC -1- FUNCTION: Membrane glycoproteins implicated in the pathologic
CC deposition of cholesterol in arterial walls during atherosclerosis.
CC Two types of receptor subunits exist. These receptors mediate the
CC endocytosis of a diverse group of macromolecules, including
CC modified low density lipoproteins (LDL).
CC -1- SUBUNIT: Homotrimer.
CC -1- SUBCELLULAR LOCATION: Type II membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Name=I;
CC IsoId=P30204-1; Sequence=Displayed;
CC Name=II;
CC IsoId=P30204-2; Sequence=VSP_006231, VSP_006232;
CC -1- SIMILARITY: Contains 1 collagen-like domain.
CC -1- SIMILARITY: Contains 1 SRCR domain.
CC
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL, L04274; AAA39747.1; ALT_INIT; mRNA.
CC EMBL, L04275; AAA39748.1; ALT_INIT; mRNA.
CC EMBL, D13382; BAA02650.1; -; mRNA.
CC EMBL, AF203781; AAF14001.1; -; mRNA.
CC EMBL, M59445; AAA37464.1; -; mRNA.
CC EMBL, M59446; AAA37465.1; -; mRNA.
CC EMBL, U13673; AAC13774.1; -; Genomic DNA.
CC EMBL, AK089178; BAC40779.1; -; mRNA.
CC EMBL, BC003814; AAH03814.1; -; mRNA.
CC PIR, B44407; B44407.
CC Ensemble; ENSMUSG00000025044; Mus musculus.
CC MGI, MGI:98257; Mri1.
CC GO, GO:0016021; C:Integral to membrane; TAS.
CC InterPro, IPR008161; C1g_helix.
CC InterPro, IPR008160; Collagen.
CC InterPro, IPR003543; Macscav_receptor.
CC InterPro, IPR002017; Spectrin.
CC InterPro, IPR001190; Scrv_receptor.
CC PANTHER, PTHR19311;SF5; Macscav_receptor; 1.
CC Pfam, PF01391; Collagen; 1.

DR Pfam: PF03523; Macscav_rec; 1.
 DR Pfam: PF00530; SRCR; 1.
 DR PRINTS; PRO1408; MACSCAVRCPR.
 DR PRINTS; PRO258; SPERACTRCPR.
 DR PRODOM; PD000007; C1g_helix; 1.
 DR PROSITE; PS00420; SRCR_1; 1.
 DR PROSITE; PS0287; SRCR_2; 1.
 KW Alternative splicing; Colled coll; Collagen; Endocytosis;
 KW Glycoprotein; Ldl; Receptor; Signal-anchor; Transmembrane.
 FT TOPO_DOM 1 55
 FT TRANSMEM 56 78
 FT TOPO_DOM 79 458
 FT DOMAIN 277 350
 FT DOMAIN 357 457
 FT REGION 79 114
 FT COILED 299 259
 FT CARBOHYD 94 94
 FT CARBOHYD 107 107
 FT CARBOHYD 147 147
 FT CARBOHYD 168 186
 FT CARBOHYD 253 253
 FT CARBOHYD 271 271
 FT DISULFID 382 446
 FT DISULFID 395 456
 FT DISULFID 426 436
 FT VARSPPLIC 352 354
 FT VARSPPLIC 355 458
 FT CONFLICT 47 47
 FT CONFLICT 110 120
 FT CONFLICT 120 130
 FT CONFLICT 130 168
 FT CONFLICT 168 202
 FT CONFLICT 202 202
 SQ SEQUENCE 458 AA; 50131 MW; 6D4C041C27EE50B CRC64;
 Query Match 38.9%; Score 801; DB 1; Length 458;
 Best Local Similarity 59.4%; Pred. No. 2.6e-40;
 Matches 158; Conservative 46; Mismatches 60; Indels 2; Gaps 2;

QY 8 PPOQBDTSCTSEKVFDAKSTVALLPPHPKNGPTLOERKSKYKALITLYLVFVLVPI 67
 DB 13 PHERDADDCSSSVFDPARSMATSLPHSTRKGPSPQEKSKKALIALIYLVFAVLIV 72
 QY 68 IGIYVAQLKMETKQCTVGSVN-ADISPEEGKNGSEDEMRPREAVMERMSNRIOY 126
 DB 73 VGIYVAQLKMETKQCTVGSVN-ADISPEEGKNGSEDEMRPREAVMERMSNRIOY 131
 QY 127 LSDNEANLIDAKNFQNFSTTTTQRRNDVLPQNLISLSIQEHENIIGDISKLVGLNTTV 186
 DB 132 ISNSKADLIDTGRFONFMSWATDORNDLILQNSILISVQEHGNSIDALSKLSQSLNMTL 191
 QY 187 LDLOSIETLNGRVQENAFKQOEEMRKLEERTLYNSAKIKSIDKQVLYEOTIKGMKML 246
 DB 192 LDVQLHTETLHVRVVESTAKQOEDISKLEERYKYSAEQVKEQDAHVEQVKEVRL 251
 QY 247 NNITNDLRKQWESQTLKNITLQOS 272
 DB 252 NNITNDLRKQWESQTLKNITFIQO 277

RESULT 7
 AVID_CHICK STANDARD; PRT; 152 AA.
 AC P02701; Q91958;
 DT *21-JUL-1996 (Rel. 01. Created)
 DT 01-NOV-1991 (Rel. 20. Last sequence update)
 DT 13-SEP-2005 (Rel. 48. Last annotation update)
 DE Avidin precursor.
 GN Name=AVID;
 OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus
 OK NCBI_TaxId=9031;
 RN (1)
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=87203184; PubMed=3575102;
 RA Gope M.L., Keinonen R.A., Kristo P.A., Connely O.M., Beattie W.G.,
 RA Zarucki-Schultz T., O'Malley B.W., Kulomaa M.S.;
 RL "Molecular cloning of the chicken egg-white avidin cDNA.",
 RL Nucleic Acids Res. 15:3595-3606 (1987).
 RN (2)
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=90355928; PubMed=2143802; DOI=10.1016/0076-6879(90)84261-E;
 RA Chandra G., Gray J.G.;
 RL "Cloning and expression of avidin in Escherichia coli.",
 RL Meth. Enzymol. 184:70-79 (1990).
 RN (3)
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=White leghorn; TISSUE=Oviduct;
 RX MEDLINE=95394357; PubMed=7665080; DOI=10.1016/0378-1119(95)00187-B;
 RA Wallen M.J., Laukanen M.O., Kulomaa M.S.;
 RL "Cloning and sequencing of the chicken egg-white avidin-encoding gene
 and its relationship with the avidin-related genes Avr1-Avr5.",
 RL Gene 161:205-209 (1995).
 RN (4)
 RP PROTEIN SEQUENCE OF 25-152. AND CARBOHYDRATE-LINKAGE SITE ASN-41.
 RX MEDLINE=71107558; PubMed=5100763;
 RA Delange R.J., Huang T.-S.;
 RL "Egg white avidin. 3. Sequence of the 78-residue middle cyanogen
 bromide peptide. Complete amino acid sequence of the protein
 subunit.",
 RL J. Biol. Chem. 246:698-709 (1971).
 RN (5)
 RP PROTEIN SEQUENCE OF 25-152. AND VARIANT THR-58.
 RX MEDLINE=71107557; PubMed=5100762;
 RA Huang T.-S., Delange R.J.;
 RL "Egg white avidin. II. Isolation, composition, and amino acid
 sequences of the tryptic peptides.",
 RL J. Biol. Chem. 246:686-697 (1971).
 RN (6)
 RP IMPORTANCE OF TYR IN BIOTIN-BINDING.
 RX MEDLINE=90351377; PubMed=2386489;
 RA Gitlin G., Bayer E.A., Wilchek M.;
 RL "Studies on the biotin-binding sites of avidin and streptavidin.
 Tyrosine residues are involved in the binding site.",
 RL Biochem. J. 269:527-530 (1990).
 RN (7)
 RP BIOTIN-BINDING STUDIES.
 RX MEDLINE=91378911; PubMed=1898347;
 RA Hiller Y., Bayer E.A., Wilchek M.;
 RL "Studies on the biotin-binding site of avidin. Minimized fragments
 that bind biotin.",
 RL Biochem. J. 278:573-585 (1991).
 RN (8)
 RP STRUCTURE OF CARBOHYDRATE.
 RX MEDLINE=83075332; PubMed=6816268;
 RA Bruch R.C., White H.B. III;
 RL "Compositional and structural heterogeneity of avidin glycopeptides.",
 RL Biochemistry 21:5334-5341 (1982).
 RN (9)
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
 RX MEDLINE=93281699; PubMed=8506353;
 RA Livnah O., Bayer E.A., Wilchek M., Sussman J.L.;
 RL "Three-dimensional structures of avidin and the avidin-biotin
 complex.",
 RL Proc. Natl. Acad. Sci. U.S.A. 90:5076-5080 (1993).
 RN (10)
 RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
 RX MEDLINE=93294833; PubMed=8515446;
 RA Pugliese L., Coda A., Malcovati M., Bolognesi M.;
 RL "Three-dimensional structure of the tetragonal crystal form of egg-
 white avidin in its functional complex with biotin at 2.7-A

RT resolution.";
 RL "J. Mol. Biol. 231:698-710(1993).
 [11]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RX MEDLINE=94430987; PubMed=9760187;
 RA Nadone E., Rosano C., Santambrogio P., Curnis F., Corti A., Magni F.,
 RA Sicaoli A.G., Paganelli G., Losso R., Aprea B., Bolognesi M.,
 RA Sicaoli A., Arosio P.;
 RT "Biochemical characterization and crystal structure of a recombinant
 hen avidin and its acidic mutant expressed in Escherichia coli.";
 RL Eur. J. Biochem. 256:453-460(1998).
 CC -1- FUNCTION: The biological function of avidin is not known. Forms a
 strong non-covalent specific complex with biotin (one molecule of
 biotin per subunit of avidin).
 CC -1- SUBUNIT: Homotetramer.
 CC -1- TISSUE SPECIFICITY: Synthesized in hen oviduct and concentrated in
 egg white (where it represent 0.05% of the total protein).
 CC -1- PTM: N-linked glycan at Asn-41 consists of GlcNAc(beta1-
 2)Man(alpha1-3)[GlcNAc(beta1-4)]Man(alpha1-6)]
 CC Man(beta1-4)GlcNAc(beta1-4)GlcNAc.
 CC -1- SIMILARITY: Belongs to the avidin/secretory protein family.
 CC -1- DATABASE: NAME=Washington enzyme manual;
 CC WWW="http://www.worthington-biochem.com/AV/".
 CC -----
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 use as long as its content is in no way modified and this statement is not
 removed.
 CC -----
 DR EMBL; X05343; CA28954.1; -; mRNA.
 DR EMBL; L27818; AAB59733.1; -; Genomic DNA.
 DR PIR; A54975; VICH.
 DR PDB; 1AVD; X-ray; A/B=25-152.
 DR PDB; 1AVB; X-ray; A/B=25-152.
 DR PDB; 1JUG; X-ray; A/B=25-152.
 DR PDB; 1LDO; X-ray; A/B=25-152.
 DR PDB; 1LDO; X-ray; A/B=25-152.
 DR PDB; 1LEL; X-ray; A/B=25-152.
 DR PDB; 1NQN; X-ray; A/B=25-147.
 DR PDB; 1RAV; X-ray; A/B=26-152.
 DR PDB; 2AVI; X-ray; A/B=25-152.
 DR PDB; 2CAM; X-ray; A/B=28-152.
 DR GLCOSuiteDB; P02701; -;
 DR Ensembl; ENSGALG0000002446; Gallus gallus.
 DR InterPro; IPR005469; Avidin.
 DR InterPro; IPR005468; Avidin/str.
 DR Pfam; PF01382; Avidin; 1.
 DR PRINTS; PR00709; AVIDIN.
 DR PROSITE; PS00577; AVIDIN; 1.
 KW 3D-structure; Biotin; Direct protein sequencing; Glycoprotein;
 KW Polymorphism; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 152 Avidin.
 FT BINDING 57 57 Biotin.
 FT CARBOHYD 41 41 N-linked (GlcNAc...).
 FT FTID=CAR_000230.
 FT DISULFID 28 107 I -> T (in about 50% of the chains).
 FT VARIANT 58 58 G -> S (in Ref. 3).
 FT CONFLICT 22 22 E -> Q (in Ref. 2 and 3).
 FT STRAND 32 36
 FT TURN 37 38
 FT STRAND 41 44
 FT TURN 49 50
 FT STRAND 52 60
 FT STRAND 68 77
 FT HELIX 80 82
 FT STRAND 87 93
 FT TURN 100 109
 FT STRAND 111 112
 FT STRAND 115 124
 FT HELIX 130 135

FT STRAND 137 146
 SQ SEQUENCE 152 AA; 16769 MW; 1D55A4491D5EFD5C CRC64;
 Query Match 32.8%; Score 675; DB 1; Length 152;
 Best Local Similarity 99.2%; Pred. No. 2.8e-33;
 Matches 127; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 273 ARKSLGKMTNDGSGNMVTIGAVNSRGEFTGTITAVATSNELKESPLHGTONTINKRT 332
 DB 25 ARKSLGKMTNDGSGNMVTIGAVNSRGEFTGTITAVATSNELKESPLHGTONTINKRT 84
 QY 333 QPTGFTVNMKFSSTVFTGQCFIDRNKKEVLKTMILLRSSVNDIGDMATRVGINIF 392
 DB 85 QPTGFTVNMKFSSTVFTGQCFIDRNKKEVLKTMILLRSSVNDIGDMATRVGINIF 144
 QY 393 TRLRTOKE 400
 DB 145 TRLRTOKE 152
 RESULT 8
 ID Q98SH4_CHICK PRELIMINARY; PRT; 152 AA.
 AC Q98SH4;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
 DE Avidin precursor.
 GN Name=AVD;
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=95394357; PubMed=7665080; DOI=10.1016/0378-1119(95)00187-B;
 RA Wallen M.J., Laakkonen M.O., Kulomaa M.S.;
 RT "Cloning and sequencing of the chicken egg-white avidin-encoding gene
 and its relationship with the avidin-related genes Avrl-Avrs.";
 RL Gene 161:205-209(1995).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=21070478; PubMed=11167523;
 RA Ahlroth M.K., Kola E.H., Ewald D., Masabanda J., Sazanov A., Fries R.,
 RA Kulomaa M.S.;
 RT "Characterization and chromosomal localization of the chicken avidin
 gene family.";
 RL Anim. Genet. 31:367-375(2000).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RA Ahlroth M.K.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ311647; CAC34569.1; -; Genomic DNA.
 DR HSSP; P02701; 1108.
 DR SMR; Q98SH4; 26-149.
 DR Ensembl; ENSGALG0000002446; Gallus gallus.
 DR InterPro; IPR005469; Avidin.
 DR InterPro; IPR005468; Avidin/str.
 DR Pfam; PF01382; Avidin; 1.
 DR PRINTS; PR00709; AVIDIN.
 DR PROSITE; PS00577; AVIDIN; 1.
 KW Signal.
 FT SIGNAL 1 24 Potential.
 SQ SEQUENCE 152 AA; 16742 MW; 04B4965B670B974B CRC64;
 Query Match 32.2%; Score 664; DB 2; Length 152;
 Best Local Similarity 97.7%; Pred. No. 1.3e-32;
 Matches 125; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 273 ARKSLGKMTNDGSGNMVTIGAVNSRGEFTGTITAVATSNELKESPLHGTONTINKRT 332
 DB 25 ARKSLGKMTNDGSGNMVTIGAVNSRGEFTGTITAVATSNELKESPLHGTONTINKRT 84

QY 333 OPTFGFTVWKKFSESTTVFTGQCFIDRNGKEVLKTMMLLRSSVNDIGDWMKATRVGINIF 392
 DB 85 OPTFGFTVWKKFSESTTVFTGQCFIDRNGKEVLKTMMLLRSSVNDIGDWMKATRVGINIF 144
 QY 393 TRLRTQKE 400
 DB 145 TRLRTQKE 152

RESULT 9

AVR4_CHICK STANDARD; PRT; 150 AA.
 ID AVR4_CHICK
 AC P56734;
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Avidin-related protein 4/5 precursor.
 GN Name=AVR4;
 GN and
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 CC NCBI_TaxID=9031;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=White Leghorn; TISSUE=Oviduct;
 RX MEDLINE=94170814; PubMed=8125122;
 RA Keinaenen R.A., Wallen M.J., Kristo P.A., Laakkonen M.O.,
 RA Toimela T.A., Helenius M.A., Kulomaa M.S.;
 RT "Molecular cloning and nucleotide sequence of chicken avidin-related
 genes 1-5."
 RL Eur. J. Biochem. 220:615-621(1994).
 CC -1- MISCELLANEOUS: The sequences of the coding regions of genes AVR4
 CC and AVR5 are identical.
 CC -1- SIMILARITY: Belongs to the avidin/streptavidin family.
 CC -----
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 CC -----
 CC EMBL, Z22883; -, NOT ANNOTATED_CDS; Genomic_DNA.
 DR PIR, S42204; S42204.
 DR PDB, 1Y52; X-ray; X/Y=25-150.
 DR PDB, 1Y53; X-ray; X/Y=25-150.
 DR PDB, 1Y55; X-ray; X/Y=25-150.
 DR SMR, P56734; 26-147.
 DR EMBL, ENSGALG0000002441; Gallus gallus.
 DR InterPro, IPR005469; Avidin.
 DR InterPro, IPR005468; Avidin/str.
 DR Pfam, PF01382; Avidin/str.
 DR PRINTS, PR00709; Avidin.
 DR PROSITE, PS00577; AVIDIN, 1.
 KM 3D-structure; Biotin; Glycoprotein; Multigene family; Signal.
 FT SIGNAL 1 24 Potential.
 FT CHAIN 25 150 Avidin-related protein 4/5.
 FT BINDING 57 57 Biotin (By similarity).
 FT CARBOHYD 67 67 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 93 93 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 141 141 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 150 AA; 16644 MW; 9A6C6C6310EF813A CRC64;
 Query Match 23.8%; Score 491; DB 1; Length 150;
 Best Local Similarity 76.6%; Pred. No. 3.7e-22;
 Matches 98; Conservative 7; Mismatches 21; Indels 2; Gaps 1;

QY 333 OPTFGFTVWKKFSESTTVFTGQCFIDRNGKEVLKTMMLLRSSVNDIGDWMKATRVGINIF 392
 DB 83 OPTFGFTVWKKFSESTTVFTGQCFIDRNGKEVLKTMMLLRSSVNDIGDWMKATRVGINIF 142
 QY 393 TRLRTQKE 400
 DB 143 TRLCTVEE 150

RESULT 10

OSAY76_MEIGA PRELIMINARY; PRT; 122 AA.
 ID OSAY76_MEIGA
 AC OSAY76;
 DT 01-MAR-2003 (TRENBLREL. 23, Created)
 DT 01-MAR-2003 (TRENBLREL. 23, Last sequence update)
 DT 01-JUN-2003 (TRENBLREL. 24, Last annotation update)
 DE Avidin (Fragment).
 OS Meleagris gallopavo (Common turkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Meleagris.
 CC NCBI_TaxID=9103;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22755852; PubMed=12672662; DOI=10.1095/biolreprod.102.015172;
 RA Long B.L., Sonstegard T.S., Long J.A., Van Tassel C.P., Zuelke K.A.;
 RT "Serial analysis of gene expression in turkey sperm storage tubules in
 RT the presence and absence of resident sperm."
 RT Biol. Reprod. 69:469-474(2003).
 DR EMBL, AF545846; AAN38297.1; -, mRNA.
 DR HSSP, P02701; INON.
 DR SMR, OSAY76; 25-122.
 DR InterPro, IPR005469; Avidin.
 DR InterPro, IPR005468; Avidin/str.
 DR Pfam, PF01382; Avidin/str.
 DR PRINTS, PR00709; AVIDIN.
 FT NON TER 122 122
 SQ SEQUENCE 122 AA; 13368 MW; 3D22EE74480B97E0 CRC64;
 Query Match 23.5%; Score 483.5; DB 2; Length 122;
 Best Local Similarity 82.9%; Pred. No. 8.1e-22;
 Matches 92; Conservative 8; Mismatches 8; Indels 3; Gaps 1;
 QY 264 LKNTLL---QGARCSLTKGKWTNDGSMNTGAVNSGEPFTGTTAVTATSNKESKSP 320
 DB 12 LLSLLALPGHSACKCLTGKWTNDGSMNTGAVNSGEPFTGTTAVTATSNKESKSP 71
 QY 321 LHTGNTINKRTPPTFGFTVWKKFSESTTVFTGQCFIDRNGKEVLKTMML 371
 DB 72 LVGTGNMINKKTPPTFGFTVWKKFSESTTVFTGQCFIDRNGKEVLKTMML 122
 RESULT 11
 AVR3_CHICK STANDARD; PRT; 150 AA.
 ID AVR3_CHICK
 AC P56733;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Avidin-related protein 3 precursor.
 GN Name=AVR3;
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 CC NCBI_TaxID=9031;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=White Leghorn; TISSUE=Oviduct;
 RX MEDLINE=94170814; PubMed=8125122;
 RA Keinaenen R.A., Wallen M.J., Kristo P.A., Laakkonen M.O.,
 RA Toimela T.A., Helenius M.A., Kulomaa M.S.;
 RT "Molecular cloning and nucleotide sequence of chicken avidin-related


```

RT genes 1-5.":
RL Bur. J. Biochem. 220:615-621(1994).
CC -1- SIMILARITY: Belongs to the avidin/streptavidin family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; Z21612; -; NOT ANNOTATED CDS; Genomic DNA.
DR EMBL; Z21536; -; NOT ANNOTATED CDS; mRNA.
DR PIR; S42203; S42203.
DR HSSP; P02701; INON.
DR SMR; P56733; 26-147.
DR Ensemble; ENSGALG0000002441; Gallus gallus.
DR InterPro; IPR005469; Avidin.
DR InterPro; IPR005468; Avidin/str.
DR Pfam; PF01382; Avidin; 1.
DR PRINTS; PR00709; Avidin.
DR PROSITE; PS00577; AVIDIN; 1.
KM Biotin; Glycoprotein; Multigene family; Signal.
FT SIGNAL 1 24
FT CHAIN 1 25
FT BINDING 57 57 Avidin-related protein 3.
FT CARBOHYD 93 93 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 141 141 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 150 AA; 16657 MW; 84DC03926A6BE21C CRC64;

Query Match 22.4%; Score 461; DB 1; Length 150;
Best Local Similarity 71.1%; Pred. No. 2.4e-20;
Matches 91; Conservative 10; Mismatches 25; Indels 2; Gaps 1;

QY 273 ARKCSLTGKMTNDGSMNTTGA VNSRGFTGTYTATVATSNETKESPLHGONTINRT 332
DB 25 ARKCSLTGKMTNDGSMNTTGA VNSRGFTGTYTATVATSNETKESPLHGONTINRT 332
QY 333 OPTGFTVNMKFSSTVFTGQC FIDRNGKEVLKTMMLRSSVNDIGDWMKATRVGINIF 392
DB 83 OPTGFTVNMKFSSTVFTGQC FIDRNGKEVLKTMMLRSSVNDIGDWMKATRVGINIF 142
QY 393 TRLRTQKE 400
DB 143 TRQRTVEE 150

RESULT 12
AVR7_CHICK STANDARD; PRT; 150 AA.
ID AVR7_CHICK
AC P56736; Q9M6V4;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Avidin-related protein 7 precursor.
GN Name=AVR7;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Rhode Island;
RX MEDLINE=21070478; PubMed=11167523;
RA Ahlroth M.K., Kola E.H., Ewald D., Meabanda J., Sazanov A., Fries R.,
RA Kulmacs M.S.;
RT "Characterization and chromosomal localization of the chicken avidin
RT gene family.";
RL Ann. Genet. 31:367-375(2000).
CC -1- SIMILARITY: Belongs to the avidin/streptavidin family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

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CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AJ237659; CAB39894.1; -; Genomic DNA.
DR HSSP; P02701; INON.
DR SMR; P56736; 26-147.
DR Ensemble; ENSGALG0000002441; Gallus gallus.
DR InterPro; IPR005469; Avidin.
DR InterPro; IPR005468; Avidin/str.
DR Pfam; PF01382; Avidin; 1.
DR PRINTS; PR00709; Avidin.
DR PROSITE; PS00577; AVIDIN; 1.
KM Biotin; Glycoprotein; Multigene family; Signal.
FT SIGNAL 1 24
FT CHAIN 1 25
FT BINDING 57 57 Avidin-related protein 7.
FT CARBOHYD 41 41 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 54 54 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 93 93 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 141 141 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 150 AA; 16543 MW; 30F335611F65923D CRC64;

Query Match 22.4%; Score 461; DB 1; Length 150;
Best Local Similarity 70.3%; Pred. No. 2.4e-20;
Matches 90; Conservative 10; Mismatches 26; Indels 2; Gaps 1;

QY 273 ARKCSLTGKMTNDGSMNTTGA VNSRGFTGTYTATVATSNETKESPLHGONTINRT 332
DB 25 ARKCSLTGKMTNDGSMNTTGA VNSRGFTGTYTATVATSNETKESPLHGONTINRT 332
QY 333 OPTGFTVNMKFSSTVFTGQC FIDRNGKEVLKTMMLRSSVNDIGDWMKATRVGINIF 392
DB 83 OPTGFTVNMKFSSTVFTGQC FIDRNGKEVLKTMMLRSSVNDIGDWMKATRVGINIF 142
QY 393 TRLRTQKE 400
DB 143 TRQRTVEE 150

RESULT 13
AVR1_CHICK STANDARD; PRT; 150 AA.
ID AVR1_CHICK
AC O13153;
DT 15-JUL-1999 (Rel. 38, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Avidin-related protein 1 precursor.
GN Name=AVR1;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Oviduct;
RX MEDLINE=88260103; PubMed=2838690; DOI=10.1016/0022-4731(88)90071-4;
RA Keinaenen R.A., Laukkanen M.-L., Kulomaa M.S.;
RT "Molecular cloning of three structurally related genes for chicken
RT avidin.";
RL J. Steroid Biochem. 30:17-21(1988).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=White Leghorn; TISSUE=Oviduct;
RX MEDLINE=94170814; PubMed=8125122;
RA Keinaenen R.A., Wallen M.J., Kristo P.A., Laukkanen M.O.,
RA Toimela T.A., Helenius M.A., Kulomaa M.S.;
RT "Molecular cloning and nucleotide sequence of chicken avidin-related
RT genes 1-5.";
RL Bur. J. Biochem. 220:615-621(1994).
CC -1- SIMILARITY: Belongs to the avidin/streptavidin family.
CC -----

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 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.

DR EMBL; 221611; -; NOT ANNOTATED CDS; Genomic_DNA.
 DR EMBL; 297063; CAB09758.1; -; mRNA.
 DR PIR; S42201; S42201.
 DR HSSP; P02701; INON.
 DR Ensembl; ENSGALG00000002441; Gallus gallus.
 DR InterPro; IPR005469; Avidin.
 DR InterPro; IPR005468; Avidin/str.
 DR Pfam; PF01382; Avidin; 1.
 DR PRINTS; PR00709; AVIDIN.
 DR PROSITE; PS00577; AVIDIN; 1.
 DR Biotin; Glycoprotein; Multigene family; Signal.
 KW SIGNAL; 1 24 Potential.
 FT CHAIN 1 25 150 Avidin-related protein 1.
 FT BINDING 57 57 Biotin (By similarity).
 FT CARBOHYD 54 54 N-linked (GlcNAc...) (potential).
 FT CARBOHYD 67 67 N-linked (GlcNAc...) (potential).
 FT CARBOHYD 93 93 N-linked (GlcNAc...) (potential).
 SQ SEQUENCE 150 AA; 16468 MW; 7754838089581F6 CRC64;

Query Match 22.0%; Score 452; DB 1; Length 150;
 Best Local Similarity 68.8%; Pred. No. 8.4e-20;
 Matches 88; Conservative 10; Mismatches 28; Indels 2; Gaps 1;

QY 273 ARKCSLTGKMTDLSNMITGAVNSRGFTGYITAVTATSNRIKESPLHGTQNTINKRT 332
 DB 25 ARKCSLTGKMDNDLSIMTIGAVNDNGENGTITAVADNPENIRSLGIQH--KRC 82

QY 333 OPTFGFTYNNKSESSTVFTGQCFIDRNGKEYLKTMTLLRSVNDIGDDWKATRVGINF 392
 DB 83 OPTFGFTYNNKSESSTVFTGQCFIDRNGKEYLKTMTLLRSVNDIGDDWKATRVGINF 142

QY 393 TRLRTQKE 400
 DB 143 TRLRTVEE 150

RESULT 14
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 ID _AVR6 CHICK STANDARD; PRT; 150 AA.
 AC P56735;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Avidin-related protein 6 precursor.
 GN Name=AVR6;
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinoptera; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OC NCBI_TaxID=9031;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Rhode Island;
 RC MEDLINE=21070478; PubMed=1167523;
 RA Ahlroth M.K., Kola E.H., Ewald D., Masabanda J., Sazanov A., Fries R.,
 RA Kulomaa M.S.;
 RT "Characterization and chromosomal localization of the chicken avidin
 RT gene family.";
 RL Ann. Genet. 31:367-375(2000).
 CC -1- SIMILARITY: Belongs to the avidin/streptavidin family.
 CC *This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.

DR EMBL; AJ237658; CAB39893.1; -; Genomic_DNA.
 DR HSSP; P02701; INON.
 DR Ensembl; ENSGALG00000002441; Gallus gallus.
 DR InterPro; IPR005469; Avidin.
 DR InterPro; IPR005468; Avidin/str.
 DR Pfam; PF01382; Avidin; 1.
 DR PRINTS; PR00709; AVIDIN.
 DR PROSITE; PS00577; AVIDIN; 1.
 DR Biotin; Glycoprotein; Multigene family; Signal.
 KW SIGNAL; 1 24 Potential.
 FT CHAIN 1 25 150 Avidin-related protein 6.
 FT BINDING 57 57 Biotin (By similarity).
 FT CARBOHYD 54 54 N-linked (GlcNAc...) (potential).
 FT CARBOHYD 93 93 N-linked (GlcNAc...) (potential).
 FT CARBOHYD 141 141 N-linked (GlcNAc...) (potential).
 SQ SEQUENCE 150 AA; 16528 MW; C0F3357D6291B150 CRC64;

Query Match 21.9%; Score 451; DB 1; Length 150;
 Best Local Similarity 68.8%; Pred. No. 9.6e-20;
 Matches 88; Conservative 11; Mismatches 27; Indels 2; Gaps 1;

QY 273 ARKCSLTGKMTDLSNMITGAVNSRGFTGYITAVTATSNRIKESPLHGTQNTINKRT 332
 DB 25 ARKCSLTGKMDNDLSIMTIGAVNDNGENGTITAVADNPENIRSLGIQH--KRC 82

QY 333 OPTFGFTYNNKSESSTVFTGQCFIDRNGKEYLKTMTLLRSVNDIGDDWKATRVGINF 392
 DB 83 OPTFGFTYNNKSESSTVFTGQCFIDRNGKEYLKTMTLLRSVNDIGDDWKATRVGINF 142

QY 393 TRLRTQKE 400
 DB 143 TRLRTVEE 150

RESULT 15
 AVR2 CHICK STANDARD; PRT; 150 AA.
 ID _AVR2 CHICK STANDARD; PRT; 150 AA.
 AC P56732; 0546L5;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Avidin-related protein 2 precursor.
 GN Name=AVR2;
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinoptera; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OC NCBI_TaxID=9031;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=White Leghorn; TISSUE=Oviduct;
 RC MEDLINE=94170814; PubMed=8125122;
 RA Keilnaenen R.A., Wallen M.J., Kistio P.A., Laukkanen M.O.,
 RA Toimela T.A., Helenus M.A., Kulomaa M.S.;
 RT "Molecular cloning and nucleotide sequence of chicken avidin-related
 RT genes 1-5.";
 RL Eur. J. Biochem. 220:615-621(1994).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RC MEDLINE=21070478; PubMed=1167523;
 RA Ahlroth M.K., Kola E.H., Ewald D., Masabanda J., Sazanov A., Fries R.,
 RA Kulomaa M.S.;
 RT "Characterization and chromosomal localization of the chicken avidin
 RT gene family.";
 RL Ann. Genet. 31:367-375(2000).
 CC -1- SIMILARITY: Belongs to the avidin/streptavidin family.
 CC *This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.

DR	EMBL; Z21554; -; NOT ANNOTATED CDS; Genomic_DNA.
DR	*EMBL; Z21535; -; NOT ANNOTATED CDS; mRNA.
DR	EMBL; AJ311648; CAC34570.1; -; Genomic_DNA.
DR	PIR; S42202; S42202.
DR	HSSP; P02701; INON.
DR	ENSEMBL; ENSGAL00000002441; Gallus gallus.
DR	InterPro; IPR005469; Avidin.
DR	InterPro; IPR005468; Avidin/str.
DR	Pfam; PF01382; Avidin; 1.
DR	PRINTS; PR00709; AVIDIN.
DR	PROSITE; PS00577; AVIDIN.
KM	Biotin; Glycoprotein; Multigene family; Signal.
FT	SIGNAL
FT	CHAIN
FT	BINDING
FT	CARBOHYD
FT	CARBOHYD
SQ	SEQUENCE

Query Match	21.2%	Score 436;	DB 1;	Length 150;
Best Local Similarity	67.2%;	Pred. No. 7.8e-19;		
Matches	86;	Conservative	11;	Mismatches 29;
			Indels	2;
			Gaps	1;

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Qy 273 ARKSLTGKWTNIGSNMTIGAVNSRGFTYITAVTATSNEIKESPLHGTONTIKRT 332
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Db 25  ARKSLTGEWMDLGSIMTIGAVNDGEPDGYITVADNPGNITISPLLGIOH--KRAS 82
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 333 OPTFETVWVKPSESTVTFPGCFIDRNGKEVLTMMLLRSSVNDIGDDMKATRVGINIF 392
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 83  OPTFETVWVNSSESTVFGOCFVDRSGKEVLTMMLLRSSVNDIGDDMIATRVGNDF 142
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Qy 393 TELRFTQKE 400
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 143 TRQHTVEE 150
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Search completed: February 16, 2006, 17:05:01
Job time : 234 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: February 16, 2006, 17:05:18 ; Search time 47 Seconds
(without alignments)
703.623 Million cell updates/sec

Title: US-10-618-570-2

Perfect score: 2059

Sequence: 1 MAQWDFPDQOEDTDSCTES.....DKATRVGINIFRLRTQKE 400

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/1aa/5_COMB.pep:*\n2: /cgn2_6/ptodata/1/1aa/6_COMB.pep:*\n3: /cgn2_6/ptodata/1/1aa/H_COMB.pep:*\n4: /cgn2_6/ptodata/1/1aa/RTUS_COMB.pep:*\n5: /cgn2_6/ptodata/1/1aa/RE_COMB.pep:*\n6: /cgn2_6/ptodata/1/1aa/backfillseq.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1381	67.1	349	6	5510466-2 Patent No. 5510466
2	1381	67.1	453	6	5510466-4 Patent No. 5510466
3	1047.5	50.9	451	1	US-08-154-365-2 Sequence 2, Appl1
4	1047.5	50.6	358	1	US-08-453-117-4 Sequence 4, Appl1
5	1047.5	50.6	358	1	US-08-948-222-4 Sequence 4, Appl1
6	1047.5	50.6	358	1	US-08-973-145-4 Sequence 4, Appl1
7	1047.5	50.6	358	4	PCT-US96-08081-4 Sequence 4, Appl1
8	1047.5	50.6	362	2	US-09-949-016-9258 Sequence 9258, Ap
9	1047.5	50.6	451	1	US-08-453-117-2 Sequence 2, Appl1
10	1047.5	50.6	451	1	US-08-948-222-2 Sequence 2, Appl1
11	1047.5	50.6	451	1	US-08-973-145-2 Sequence 2, Appl1
12	1047.5	50.6	451	2	US-09-276-400-10 Sequence 10, Appl
13	1047.5	50.6	451	2	US-09-448-076-10 Sequence 10, Appl
14	1047.5	50.6	451	2	US-09-702-572-10 Sequence 10, Appl
15	1047.5	50.6	451	4	PCT-US96-08081-2 Sequence 2, Appl1
16	678	32.9	152	2	US-08-831-399-4 Sequence 4, Appl1
17	678	32.9	152	2	US-09-366-862-4 Sequence 4, Appl1
18	678	32.9	152	2	US-09-368-772-4 Sequence 4, Appl1
19	138.5	6.7	159	2	US-08-628-540-1 Sequence 1, Appl1
20	138.5	6.7	159	2	US-08-948-097-17 Sequence 17, Appl1
21	138.5	6.7	159	2	US-08-941-100-1 Sequence 1, Appl1
22	138.5	6.7	159	2	US-08-941-100-5 Sequence 5, Appl1
23	138.5	6.7	159	2	US-09-381-430-2 Sequence 2, Appl1
24	138.5	6.7	159	2	US-08-831-399-2 Sequence 2, Appl1
25	138.5	6.7	183	2	US-09-366-862-2 Sequence 2, Appl1
26	138.5	6.7	183	2	US-09-368-772-2 Sequence 2, Appl1
27	138.5	6.7	183	4	PCT-US93-05240-14 Sequence 14, Appl1

28	138.5	6.7	183	6	5168049-5 Patent No. 5168049
29	138.5	6.7	415	1	US-08-491-988-7 Sequence 7, Appl1
30	138.5	6.7	421	2	US-09-938-2708-1 Sequence 1, Appl1
31	138.5	6.7	435	1	US-08-491-988-5 Sequence 5, Appl1
32	138.5	6.6	128	1	US-08-211-833-2 Sequence 2, Appl1
33	135.5	6.6	128	1	US-08-434-718-2 Sequence 2, Appl1
34	135.5	6.6	128	2	US-08-831-399-16 Sequence 16, Appl
35	135.5	6.6	128	2	US-09-366-862-16 Sequence 16, Appl
36	135.5	6.6	128	2	US-09-368-772-16 Sequence 16, Appl
37	135.5	6.6	402	1	US-08-491-988-9 Sequence 9, Appl1
38	135.5	6.6	10182	2	US-09-134-001C-3159 Sequence 3159, Ap
39	133	6.5	186	2	US-09-382-276-2 Sequence 2, Appl1
40	132.5	6.4	118	2	US-07-780-717C-7 Sequence 7, Appl1
41	131	6.4	186	2	US-09-382-276-3 Sequence 3, Appl1
42	130.5	6.3	183	2	US-09-382-276-1 Sequence 1, Appl1
43	130.5	6.3	183	2	US-09-285-867-1 Sequence 1, Appl1
44	129.5	6.3	1307	2	US-09-949-016-7561 Sequence 7561, Ap
45	123	6.0	2663	2	US-09-538-092-1252 Sequence 1252, Ap

ALIGNMENTS

```

RESULT 1
5510466-2
; Patent No. 5510466
; APPLICANT: KREIGER, MONTY; KODAMA, TATSUHIKO
; TITLE OF INVENTION: SCAVENGER RECEPTOR PROTEIN AND ANTIBODY
; THERETO
; NUMBER OF SEQUENCES: 12
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/307,400
; FILING DATE: 16-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 997,113
; FILING DATE: 24-DEC-1992
; APPLICATION NUMBER: 391,486
; FILING DATE: 09-AUG-1989
; APPLICATION NUMBER: 272,002
; FILING DATE: 15-NOV-1988
; SEQ ID NO:2:
; LENGTH: 349
5510466-2

Query Match      67.1%; Score 1381; DB 6; Length 349;
Best Local Similarity 100.0%; Pred. No. 4.3e-112; Indels 0; Gaps 0;
Matches 272; Conservative 0; Mismatches 0;

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DB      1 MAQWDFPDQOEDTDSCTESYKFDARSVTALLPFPKKGPTLOERMKSXTALTITLYLV 60

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QY      61 FVVLPIIIGIYAQAQLKMETKNCCTGVSNADISPSPEKKGSGEDEMRPREAVERMSNM 120
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DB      61 FVVLPIIIGIYAQAQLKMETKNCCTGVSNADISPSPEKKGSGEDEMRPREAVERMSNM 120

QY      121 ESRIOYLSDNENANLIDAKNFQNFSTTQRRNDVLFQANSLSSIOEHENITIGDISKLV 180
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DB      121 ESRIOYLSDNENANLIDAKNFQNFSTTQRRNDVLFQANSLSSIOEHENITIGDISKLV 180

QY      121 ESRIOYLSDNENANLIDAKNFQNFSTTQRRNDVLFQANSLSSIOEHENITIGDISKLV 180
      |||
DB      121 ESRIOYLSDNENANLIDAKNFQNFSTTQRRNDVLFQANSLSSIOEHENITIGDISKLV 180

QY      181 GANTTVLLOFSIETLNGRVOENAFKQOEBRKLEERYLYNSAEIKSIDKQVYLEQIRK 240
      |||
DB      181 GANTTVLLOFSIETLNGRVOENAFKQOEBRKLEERYLYNSAEIKSIDKQVYLEQIRK 240

QY      241 GEMKLNITNDRLRKDWEHSQTLKNITLLOG 272
      |||
DB      241 GEMKLNITNDRLRKDWEHSQTLKNITLLOG 272

RESULT 2
5510466-4
; Patent No. 5510466
; APPLICANT: KREIGER, MONTY; KODAMA, TATSUHIKO

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TITLE OF INVENTION: SCAVENGER RECEPTOR PROTEIN AND ANTIBODY
THREETO
NUMBER OF SEQUENCES: 12
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/307,400
FILING DATE: 16-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 997,113
FILING DATE: 24-DEC-1992
APPLICATION NUMBER: 391,486
FILING DATE: 09-AUG-1989
APPLICATION NUMBER: 272,002
FILING DATE: 15-NOV-1988
SEQ ID NO: 4
LENGTH: 453
5510466-4

Query Match 67.1%; Score 1381; DB 6; Length 453;
Best Local Similarity 100.0%; Pred. No. 6,3e-112;
Matches 272; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQMDPPDQEDTDSCTESYKFDARSVTALLPFPKNGPTLOERMSYKATLITLYLV 60
DB 1 MAQMDPPDQEDTDSCTESYKFDARSVTALLPFPKNGPTLOERMSYKATLITLYLV 60

QY 61 FVVLVPIIGIYAAOLLKMETKNCCTGVSNADISPSPEKGNGSEDEMRPREAVMERMSNM 120
DB 61 FVVLVPIIGIYAAOLLKMETKNCCTGVSNADISPSPEKGNGSEDEMRPREAVMERMSNM 120

QY 121 ESRIOYLSDENEANLIDAKNFONFSITTDQRFNDVLFOQLNSLLSIOEHENIIGDISKSLV 180
DB 121 ESRIOYLSDENEANLIDAKNFONFSITTDQRFNDVLFOQLNSLLSIOEHENIIGDISKSLV 180

QY 181 GIANTTVLDLOFSIETTLNGRVQENAFKQOEEMRKLEERTYNSAEIKSLDEKQVYLEQEI 240
DB 181 GIANTTVLDLOFSIETTLNGRVQENAFKQOEEMRKLEERTYNSAEIKSLDEKQVYLEQEI 240

QY 241 GEMKLNITNDRLKDMESHOTLKNITLLQG 272
DB 241 GEMKLNITNDRLKDMESHOTLKNITLLQG 272

RESULT 3
US-08-154-365-2
Sequence 2, Application US/08154365
Patent No. 5624904
GENERAL INFORMATION:
APPLICANT: Dunne, Dana W.
APPLICANT: Resnick, David
APPLICANT: Kreiger, Monty
APPLICANT: Joiner, Keith A.
TITLE OF INVENTION: Method for Treating Gram-Positive
TITLE OF INVENTION: Septicemia
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 1100 Peachtree Street, Suite 2800
CITY: Atlanta
STATE: Ga
COUNTRY: USA
ZIP: 30309-4530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/154,365
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284

REFERENCE/DOCKET NUMBER: MIT6392
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-815-6508
TELEFAX: (404)-815-6555
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 451 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: homo sapien
PUBLICATION INFORMATION:
AUTHORS: Ashkenas, et al.
JOURNAL: J. Lipid Res.
VOLUME: 34
PAGES: 983-1000
DATE: 1993
RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 451
US-08-154-365-2

Query Match 50.9%; Score 1047.5; DB 1; Length 451;
Best Local Similarity 72.5%; Pred. No. 7.4e-83;
Matches 198; Conservative 40; Mismatches 34; Indels 1; Gaps 1;

QY 1 MAQMDPPDQEDTDSCTESYKFDARSVTALLPFPKNGPTLOERMSYKATLITLYLV 60
DB 1 MEQMDHFHQOEDTDSCTESYKFDARSVTALLPFPKNGPTLOERMSYKATLITLYLV 60

QY 61 FVVLVPIIGIYAAOLLKMETKNCCTGVSNADISPSPEKGNGSEDEMRPREAVMERMSNM 119
DB 61 FVVLVPIIGIYAAOLLKMETKNCCTGVSNADISPSPEKGNGSEDEMRPREAVMERMSNM 120

QY 120 MESRIOYLSDENEANLIDAKNFONFSITTDQRFNDVLFOQLNSLLSIOEHENIIGDISKSL 179
DB 120 MESRIOYLSDENEANLIDAKNFONFSITTDQRFNDVLFOQLNSLLSIOEHENIIGDISKSL 180

QY 181 GIANTTVLDLOFSIETTLNGRVQENAFKQOEEMRKLEERTYNSAEIKSLDEKQVYLEQEI 239
DB 181 ISLNTTVLDLOFSIETTLNGRVQENAFKQOEEMRKLEERTYNSAEIKSLDEKQVYLEQEI 240

QY 240 GEMKLNITNDRLKDMESHOTLKNITLLQG 272
DB 241 GEMKLNITNDRLKDMESHOTLKNITLLQG 273

RESULT 4
US-08-453-117-4
Sequence 4, Application US/08453117
Patent No. 5683903
GENERAL INFORMATION:
APPLICANT: Lyoko, Paul G.
APPLICANT: Elshourbagy, Nabli A.
APPLICANT: Branner, Mary E.
TITLE OF INVENTION: Attachment Enhanced 293 Cells
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: U.S.
STREET: Mailcode - UM2220, 709 Swedeland Road
CITY: King of Prussia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19406-5090
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30

```

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,117
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jervis, Herbert H.
REGISTRATION NUMBER: 31,171
REFERENCE/DOCKET NUMBER: SBC-P50338
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 270-5019
TELEFAX: (610) 270-5090
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-453-117-4

Query Match      50.6%; Score 1042.5; DB 1; Length 358;
Best Local Similarity 72.2%; Pred. No. 1.4e-82;
Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;

QY 1 MAQMDPFDQOEDTSCSYKFDARSVTALLPPHPKNGPTIOEEMKSYKTLITLYLV 60
DB 1 MEQWDFHNOQEDTSCSYKFDARSMTALLPPHPKNSPSIOEKLKSKFALLIYLV 60
QY 61 FVVLPIIGIYVAOQLKMKETKCTGVSA-VNA-DISPSPEKGSGSEDEMRFREAVERN 119
DB 61 FAVLPIIGIYVAOQLKMKETKCTGVSA-VNA-DISPSPEKGSGSEDEMRFREAVERN 120
QY 120 MESRIQYLSDNENALLDANKFONFSITTDORFNDVLPOLNSLSSIOEHENIIGDISKL 179
DB 121 MEKRIQHLIDENALMDTEHFONFSMTTDORFNDVLPOLNSLSSIOEHENIIGDISKL 180
QY 180 VGLNTTVLDLOFSITLNGRVOENAFKQOEEMKLEERYNYSAEIKSLDEKQVLEOEI 239
DB 181 ISLNTTLLDLOINENLNGKIQENTFKQOEISKEERYNYSAEIMAKEQVHLEOEI 240
QY 240 KGEMLNNITNDLRKDEHESQTLKNITLLQG 272
DB 241 KGEVYLVNITNDLRKDEHESQTLKNITLLQG 273

RESULT 5
US-08-948-222-4
Sequence 4, Application US/08948222
Patent No. 5863798
GENERAL INFORMATION:
APPLICANT: Lyeko, Paul G.
APPLICANT: Eishourbagy, Nabli A.
APPLICANT: Brauner, Mary B.
TITLE OF INVENTION: Attachment Enhanced 293 Cells
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSER: Smithkline Beecham - Corporate Patents
ADDRESSER: U.S.
CITY: King of Prussia
STREET: Mailcode - UW2220, 709 Swedeland Road
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19406-5090
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/948,222
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/453,117
```

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FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Jervis, Herbert H.
REGISTRATION NUMBER: 31,171
REFERENCE/DOCKET NUMBER: SBC-P50338
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 270-5019
TELEFAX: (610) 270-5090
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-948-222-4

Query Match      50.6%; Score 1042.5; DB 1; Length 358;
Best Local Similarity 72.2%; Pred. No. 1.4e-82;
Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;

QY 1 MAQMDPFDQOEDTSCSYKFDARSVTALLPPHPKNGPTIOEEMKSYKTLITLYLV 60
DB 1 MEQWDFHNOQEDTSCSYKFDARSMTALLPPHPKNSPSIOEKLKSKFALLIYLV 60
QY 61 FVVLPIIGIYVAOQLKMKETKCTGVSA-VNA-DISPSPEKGSGSEDEMRFREAVERN 119
DB 61 FAVLPIIGIYVAOQLKMKETKCTGVSA-VNA-DISPSPEKGSGSEDEMRFREAVERN 120
QY 120 MESRIQYLSDNENALLDANKFONFSITTDORFNDVLPOLNSLSSIOEHENIIGDISKL 179
DB 121 MEKRIQHLIDENALMDTEHFONFSMTTDORFNDVLPOLNSLSSIOEHENIIGDISKL 180
QY 180 VGLNTTVLDLOFSITLNGRVOENAFKQOEEMKLEERYNYSAEIKSLDEKQVLEOEI 239
DB 181 ISLNTTLLDLOINENLNGKIQENTFKQOEISKEERYNYSAEIMAKEQVHLEOEI 240
QY 240 KGEMLNNITNDLRKDEHESQTLKNITLLQG 272
DB 241 KGEVYLVNITNDLRKDEHESQTLKNITLLQG 273

RESULT 6
US-08-973-145-4
Sequence 4, Application US/08973145
Patent No. 5919636
GENERAL INFORMATION:
APPLICANT: Lyeko, Paul G.
APPLICANT: Eishourbagy, Nabli A.
APPLICANT: Brauner, Mary B.
TITLE OF INVENTION: Attachment Enhanced 293 Cells
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSER: Smithkline Beecham - Corporate Patents U.S.
ADDRESSER: Mailcode - UW2220, 709 Swedeland Road
CITY: King of Prussia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19406-5090
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,145
FILING DATE: 26-NOV-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth J. Hecht
REGISTRATION NUMBER: P-41, 824
REFERENCE/DOCKET NUMBER: P50338
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 270-5009
```

TELEFAX: (610) 270-5090
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 358 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-973-145-4

Query Match 50.6%; Score 1042.5; DB 1; Length 358;
 Best Local Similarity 72.2%; Pred. No. 1.4e-82;
 Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;

QY 1 MAQMDPDPQOEDPDSCTESVYKFDARSVTALLPPHPKGPPTLOEMKSYKTALLTYLYIV 60
 DB 1 MEQMDHPNQOEDPDSCTESVYKFDARSMTALLPPHPKSPSLQEKLSFKKALLTYLYIV 60
 QY 61 FVLVPIIGIYVAOQLKMETKCTVGSVNA-DISPSPEKGNGSEDEMRPREAVEMRSN 119
 DB 61 FVLVPIIGIYVAOQLKMETKCTVGSVNA-DISPSPEKGNGSEDEMRPREAVEMRSN 120
 QY 120 MESRIQYISDNEANILDAKNFONFSITTDQRFNDVLPOLNSLSIOEHENIGDISKSL 179
 DB 121 MEKRIQHILDEANILMDTEHPONFSMTTDQRFNDILQLSTLFSVQGHNAIDETSKSL 180
 QY 180 VGLNTTVLDLQFSIETLNGRVOENAFKQOEMKLEERINYASAEIKSLDEKQVLEBEI 239
 DB 181 ISLNTTLLDLQNLINENLNGKIQENTFKQOEBISKLEERVYVNSAIVAMKEQVHLEBEI 240
 QY 240 KGEKMLNNITNDRLKDMESQTLKNITTLQ 272
 DB 241 KGEVAVLNNITNDRLKDMESQTLKNITTLQ 273

RESULT 7

PCT-US96-08081-4
 Sequence 4, Application PC/TUS9608081
 GENERAL INFORMATION:
 APPLICANT: SmithKline Beecham Corporation
 TITLE OF INVENTION: Attachment Enhanced 293 Cells
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SmithKline Beecham - Corporate Patents U.S.
 STREET: Mailcode - UM2220, 709 Swedeland Road
 CITY: King of Prussia
 STATE: Pennsylvania
 COUNTRY: U.S.A.
 ZIP: 19406-5030
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US96/08081
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Jerry's, Herbert H.
 REGISTRATION NUMBER: 31,171
 REFERENCE/DOCKET NUMBER: P50338
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (610) 270-5019
 TELEFAX: (610) 270-5090
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 358 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 PCT-US96-08081-4

Query Match 50.6%; Score 1042.5; DB 4; Length 358;

Best Local Similarity 72.2%; Pred. No. 1.4e-82;
 Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;

QY 1 MAQMDPDPQOEDPDSCTESVYKFDARSVTALLPPHPKGPPTLOEMKSYKTALLTYLYIV 60
 DB 1 MEQMDHPNQOEDPDSCTESVYKFDARSMTALLPPHPKSPSLQEKLSFKKALLTYLYIV 60
 QY 61 FVLVPIIGIYVAOQLKMETKCTVGSVNA-DISPSPEKGNGSEDEMRPREAVEMRSN 119
 DB 61 FVLVPIIGIYVAOQLKMETKCTVGSVNA-DISPSPEKGNGSEDEMRPREAVEMRSN 120
 QY 120 MESRIQYISDNEANILDAKNFONFSITTDQRFNDVLPOLNSLSIOEHENIGDISKSL 179
 DB 121 MEKRIQHILDEANILMDTEHPONFSMTTDQRFNDILQLSTLFSVQGHNAIDETSKSL 180
 QY 180 VGLNTTVLDLQFSIETLNGRVOENAFKQOEMKLEERINYASAEIKSLDEKQVLEBEI 239
 DB 181 ISLNTTLLDLQNLINENLNGKIQENTFKQOEBISKLEERVYVNSAIVAMKEQVHLEBEI 240
 QY 240 KGEKMLNNITNDRLKDMESQTLKNITTLQ 272
 DB 241 KGEVAVLNNITNDRLKDMESQTLKNITTLQ 273

RESULT 8

US-09-949-016-9258
 Sequence 9258, Application US/09949016
 Patent No. 6812339
 GENERAL INFORMATION:
 APPLICANT: VENTER, J. Craig et al.
 TITLE OF INVENTION: POLYNORPHISMS IN KNOWN GENES ASSOCIATED
 WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CLO01307
 CURRENT APPLICATION NUMBER: US/09/949,016
 CURRENT FILING DATE: 2000-04-14
 PRIOR APPLICATION NUMBER: 60/241,755
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/237,768
 PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: 60/231,498
 PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 207012
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 9258
 LENGTH: 362
 TYPE: PRT
 ORGANISM: Human
 US-09-949-016-9258

Query Match 50.6%; Score 1042.5; DB 2; Length 362;
 Best Local Similarity 72.2%; Pred. No. 1.5e-82;
 Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;

QY 1 MAQMDPDPQOEDPDSCTESVYKFDARSVTALLPPHPKGPPTLOEMKSYKTALLTYLYIV 60
 DB 5 MEQMDHPNQOEDPDSCTESVYKFDARSMTALLPPHPKSPSLQEKLSFKKALLTYLYIV 64
 QY 61 FVLVPIIGIYVAOQLKMETKCTVGSVNA-DISPSPEKGNGSEDEMRPREAVEMRSN 119
 DB 65 FVLVPIIGIYVAOQLKMETKCTVGSVNA-DISPSPEKGNGSEDEMRPREAVEMRSN 124
 QY 120 MESRIQYISDNEANILDAKNFONFSITTDQRFNDVLPOLNSLSIOEHENIGDISKSL 179
 DB 125 MEKRIQHILDEANILMDTEHPONFSMTTDQRFNDILQLSTLFSVQGHNAIDETSKSL 184
 QY 180 VGLNTTVLDLQFSIETLNGRVOENAFKQOEMKLEERINYASAEIKSLDEKQVLEBEI 239
 DB 185 ISLNTTLLDLQNLINENLNGKIQENTFKQOEBISKLEERVYVNSAIVAMKEQVHLEBEI 244
 QY 240 KGEKMLNNITNDRLKDMESQTLKNITTLQ 272
 DB 245 KGEVAVLNNITNDRLKDMESQTLKNITTLQ 277

RESULT 9

US-08-453-117-2

Sequence 2, Application US/08453117

Patent No. 5683903

GENERAL INFORMATION:

APPLICANT: Lysko, Paul G.

APPLICANT: Elshourbagy, Nabil A.

APPLICANT: Brainer, Mary E.

TITLE OF INVENTION: Attachment Enhanced 293 Cells

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESS: SmithKline Beecham - Corporate Patents

ADDRESS: U.S.

STREET: Mallcode - UW2220, 709 Swedeland Road

CITY: King of Prussia

STATE: Pennsylvania

COUNTRY: U.S.A.

ZIP: 19406-5090

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/453,117

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Jarvis, Herbert H.

REGISTRATION NUMBER: 31,171

REFERENCE/DOCKET NUMBER: SBC-P50338

TELEPHONE: (610) 270-5019

TELEFAX: (610) 270-5090

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 451 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-453-117-2

Query Match

Best Local Similarity 72.2%; Score 1042.5; DB 1; Length 451;

Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;

QY 1 MAQWDPDPPQDEDTSCSSEVFKFADARSVTALLPPHPKNGPTLOERKSKYKALTITLYLV 60

1 MEQWDFHFNQDEDTSCSSEVFKFADARSVTALLPPHPKNGPTLOERKSKYKALTITLYLV 60

QY 61 FVLLVPIIGIIVAQAOLKMKETKCTGVSVA-DISPSPEGKNGSDEMRPREAVERMSN 119

61 FVLLVPIIGIIVAQAOLKMKETKCTGVSVA-DISPSPEGKNGSDEMRPREAVERMSN 119

DB 61 FVLLVPIIGIIVAQAOLKMKETKCTGVSVA-DISPSPEGKNGSDEMRPREAVERMSN 120

QY 120 MESRIQVSDNENANLIDAKNFONFSTTTDORFNDVLFQINSLSLSIOEHENIIGDISKSL 179

120 MESRIQVSDNENANLIDAKNFONFSTTTDORFNDVLFQINSLSLSIOEHENIIGDISKSL 179

DB 121 MEKRIQVSDNENANLIDAKNFONFSTTTDORFNDVLFQINSLSLSIOEHENIIGDISKSL 180

QY 180 VGLNTTVLDLQINLEINLNGIKQENTFKQOEBSKLEERYNVASAIIMAKEQVHLEQEI 239

180 VGLNTTVLDLQINLEINLNGIKQENTFKQOEBSKLEERYNVASAIIMAKEQVHLEQEI 239

DB 181 ISLNTTVLDLQINLEINLNGIKQENTFKQOEBSKLEERYNVASAIIMAKEQVHLEQEI 240

QY 240 KGEVKLVANNITNDLRKDKWEHSQTLRNITLIG 272

240 KGEVKLVANNITNDLRKDKWEHSQTLRNITLIG 272

DB 241 KGEVKLVANNITNDLRKDKWEHSQTLRNITLIG 273

RESULT 10

US-08-948-222-2

Sequence 2, Application US/08948222

Patent No. 5863798

GENERAL INFORMATION:

APPLICANT: Lysko, Paul G.

APPLICANT: Elshourbagy, Nabil A.

APPLICANT: Brainer, Mary E.

TITLE OF INVENTION: Attachment Enhanced 293 Cells

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESS: SmithKline Beecham - Corporate Patents

ADDRESS: U.S.

STREET: Mallcode - UW2220, 709 Swedeland Road

CITY: King of Prussia

STATE: Pennsylvania

COUNTRY: U.S.A.

ZIP: 19406-5090

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/453,117

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Jarvis, Herbert H.

REGISTRATION NUMBER: 31,171

REFERENCE/DOCKET NUMBER: SBC-P50338

TELEPHONE: (610) 270-5019

TELEFAX: (610) 270-5090

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 451 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-948-222-2

Query Match

Best Local Similarity 72.2%; Score 1042.5; DB 1; Length 451;

Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;

QY 1 MAQWDPDPPQDEDTSCSSEVFKFADARSVTALLPPHPKNGPTLOERKSKYKALTITLYLV 60

1 MEQWDFHFNQDEDTSCSSEVFKFADARSVTALLPPHPKNGPTLOERKSKYKALTITLYLV 60

QY 61 FVLLVPIIGIIVAQAOLKMKETKCTGVSVA-DISPSPEGKNGSDEMRPREAVERMSN 119

61 FVLLVPIIGIIVAQAOLKMKETKCTGVSVA-DISPSPEGKNGSDEMRPREAVERMSN 119

DB 61 FVLLVPIIGIIVAQAOLKMKETKCTGVSVA-DISPSPEGKNGSDEMRPREAVERMSN 120

QY 120 MESRIQVSDNENANLIDAKNFONFSTTTDORFNDVLFQINSLSLSIOEHENIIGDISKSL 179

120 MESRIQVSDNENANLIDAKNFONFSTTTDORFNDVLFQINSLSLSIOEHENIIGDISKSL 179

DB 121 MEKRIQVSDNENANLIDAKNFONFSTTTDORFNDVLFQINSLSLSIOEHENIIGDISKSL 180

QY 180 VGLNTTVLDLQINLEINLNGIKQENTFKQOEBSKLEERYNVASAIIMAKEQVHLEQEI 239

180 VGLNTTVLDLQINLEINLNGIKQENTFKQOEBSKLEERYNVASAIIMAKEQVHLEQEI 239

DB 181 ISLNTTVLDLQINLEINLNGIKQENTFKQOEBSKLEERYNVASAIIMAKEQVHLEQEI 240

QY 240 KGEVKLVANNITNDLRKDKWEHSQTLRNITLIG 272

240 KGEVKLVANNITNDLRKDKWEHSQTLRNITLIG 272

DB 241 KGEVKLVANNITNDLRKDKWEHSQTLRNITLIG 273

APPLICANT: Lysko, Paul G.

APPLICANT: Elshourbagy, Nabil A.

APPLICANT: Brainer, Mary E.

TITLE OF INVENTION: Attachment Enhanced 293 Cells

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESS: SmithKline Beecham - Corporate Patents

ADDRESS: U.S.

STREET: Mallcode - UW2220, 709 Swedeland Road

CITY: King of Prussia

STATE: Pennsylvania

COUNTRY: U.S.A.

ZIP: 19406-5090

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/948,222

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/453,117

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Jarvis, Herbert H.

REGISTRATION NUMBER: 31,171

REFERENCE/DOCKET NUMBER: SBC-P50338

TELEPHONE: (610) 270-5019

TELEFAX: (610) 270-5090

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 451 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-948-222-2

Query Match

Best Local Similarity 72.2%; Score 1042.5; DB 1; Length 451;

Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;

QY 1 MAQWDPDPPQDEDTSCSSEVFKFADARSVTALLPPHPKNGPTLOERKSKYKALTITLYLV 60

1 MEQWDFHFNQDEDTSCSSEVFKFADARSVTALLPPHPKNGPTLOERKSKYKALTITLYLV 60

QY 61 FVLLVPIIGIIVAQAOLKMKETKCTGVSVA-DISPSPEGKNGSDEMRPREAVERMSN 119

61 FVLLVPIIGIIVAQAOLKMKETKCTGVSVA-DISPSPEGKNGSDEMRPREAVERMSN 119

DB 61 FVLLVPIIGIIVAQAOLKMKETKCTGVSVA-DISPSPEGKNGSDEMRPREAVERMSN 120

QY 120 MESRIQVSDNENANLIDAKNFONFSTTTDORFNDVLFQINSLSLSIOEHENIIGDISKSL 179

120 MESRIQVSDNENANLIDAKNFONFSTTTDORFNDVLFQINSLSLSIOEHENIIGDISKSL 179

DB 121 MEKRIQVSDNENANLIDAKNFONFSTTTDORFNDVLFQINSLSLSIOEHENIIGDISKSL 180

QY 180 VGLNTTVLDLQINLEINLNGIKQENTFKQOEBSKLEERYNVASAIIMAKEQVHLEQEI 239

180 VGLNTTVLDLQINLEINLNGIKQENTFKQOEBSKLEERYNVASAIIMAKEQVHLEQEI 239

DB 181 ISLNTTVLDLQINLEINLNGIKQENTFKQOEBSKLEERYNVASAIIMAKEQVHLEQEI 240

QY 240 KGEVKLVANNITNDLRKDKWEHSQTLRNITLIG 272

240 KGEVKLVANNITNDLRKDKWEHSQTLRNITLIG 272

DB 241 KGEVKLVANNITNDLRKDKWEHSQTLRNITLIG 273

RESULT 11

US-08-973-145-2

Sequence 2, Application US/08973145

Patent No. 5919636

GENERAL INFORMATION:

APPLICANT: Lysko, Paul G.

APPLICANT: Elshourbagy, Nabil A.

APPLICANT: Brainer, Mary E.

TITLE OF INVENTION: Attachment Enhanced 293 Cells

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESS: SmithKline Beecham - Corporate Patents

ADDRESS: U.S.

STREET: Mallcode - UW2220, 709 Swedeland Road

CITY: King of Prussia

STATE: Pennsylvania

COUNTRY: U.S.A.

ZIP: 19406-5090

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/948,222

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/453,117

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Jarvis, Herbert H.

REGISTRATION NUMBER: 31,171

REFERENCE/DOCKET NUMBER: SBC-P50338

TELEPHONE: (610) 270-5019

TELEFAX: (610) 270-5090

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 451 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-948-222-2

Query Match

Best Local Similarity 72.2%; Score 1042.5; DB 1; Length 451;

Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;

QY 1 MAQWDPDPPQDEDTSCSSEVFKFADARSVTALLPPHPKNGPTLOERKSKYKALTITLYLV 60

1 MEQWDFHFNQDEDTSCSSEVFKFADARSVTALLPPHPKNGPTLOERKSKYKALTITLYLV 60

QY 61 FVLLVPIIGIIVAQAOLKMKETKCTGVSVA-DISPSPEGKNGSDEMRPREAVERMSN 119

61 FVLLVPIIGIIVAQAOLKMKETKCTGVSVA-DISPSPEGKNGSDEMRPREAVERMSN 119

DB 61 FVLLVPIIGIIVAQAOLKMKETKCTGVSVA-DISPSPEGKNGSDEMRPREAVERMSN 120

QY 120 MESRIQVSDNENANLIDAKNFONFSTTTDORFNDVLFQINSLSLSIOEHENIIGDISKSL 179

120 MESRIQVSDNENANLIDAKNFONFSTTTDORFNDVLFQINSLSLSIOEHENIIGDISKSL 179

DB 121 MEKRIQVSDNENANLIDAKNFONFSTTTDORFNDVLFQINSLSLSIOEHENIIGDISKSL 180

QY 180 VGLNTTVLDLQINLEINLNGIKQENTFKQOEBSKLEERYNVASAIIMAKEQVHLEQEI 239

180 VGLNTTVLDLQINLEINLNGIKQENTFKQOEBSKLEERYNVASAIIMAKEQVHLEQEI 239

DB 181 ISLNTTVLDLQINLEINLNGIKQENTFKQOEBSKLEERYNVASAIIMAKEQVHLEQEI 240

QY 240 KGEVKLVANNITNDLRKDKWEHSQTLRNITLIG 272

240 KGEVKLVANNITNDLRKDKWEHSQTLRNITLIG 272

DB 241 KGEVKLVANNITNDLRKDKWEHSQTLRNITLIG 273

TITLE OF INVENTION: Attachment Enhanced 293 Cells
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SmithKline Beecham - Corporate Patents U.S.
 STREET: Mailcode - UW2220, 709 Swedeland Road
 CITY: King of Prussia
 STATE: Pennsylvania
 COUNTRY: U.S.A.
 ZIP: 19406-5090
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/973,145
 FILING DATE: 26-NOV-1997
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Elizabeth J. Hecht
 REGISTRATION NUMBER: P-41, 824
 REFERENCE/DOCKET NUMBER: P50338
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (610) 270-5009
 TELEFAX: (610) 270-5090
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 451 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-973-145-2

Query Match 50.6%; Score 1042.5; DB 1; Length 451;
 Best Local Similarity 72.2%; Pred. No. 2e-82; Indels 1; Gaps 1;
 Matches 197; Conservative 41; Mismatches 34;

QY 1 MAQWDPDQOEDTDSCTESVYKFDARSVTALLPPHPKNGPTLOERKSKYKATLITLYLIV 60
 DB 1 MEQWDFHNOQEDTDSCTESVYKFDARSMTALLPPHPKNSPSIQETLKSFKALLIALYLLV 60
 QY 61 FVVLVPIIGIYAAQLKMETKNCCTVGSVNA-DISSPBGKNGSGDEMRFRFAVVERNSN 119
 DB 61 FAVLIPILIGIYAAQLKMETKNCSSVSTNANDITQSLTGKNDSEEMRFOEFVMEHNSN 120
 QY 120 MESRIQYSDNEANLIDAKNFONFSITTDQRFNDVLPOLNSLSIOEHENIIGDISKL 179
 DB 121 MEKRIQHLIDNEANLMDTEHFONFSMTTDQRFNDILQLSTLFSVOGHNAIDISKL 180
 QY 180 VGLNTTVLDLQFSIETTLNGRVOENAFKQOEMRKLEERIYNASAEIKSLDEKQVYLEOEI 239
 DB 181 ISLNTTLLDLQNLINENLNGKIQENTFKQOEISKLEERYVNVSAIIMAKKEQVHLEOEI 240
 QY 240 KGEKMLNNITNDRLKDMESQTLKNTITLQ 272
 DB 241 KGEVAVLNNITNDRLKDMESQTLKNTITLQ 273

RESULT 12
 US-09-276-400-10
 Sequence 10, Application US/09276400
 Patent No. 6140056
 GENERAL INFORMATION:
 APPLICANT: Khodadoust, Mehran
 TITLE OF INVENTION: NOVEL MSP-18 PROTEIN AND NUCLEIC ACID MOLECULES AND
 TITLE OF INVENTION: USES THEREFOR
 FILE REFERENCE: WNI-073
 CURRENT APPLICATION NUMBER: US/09/276,400
 CURRENT FILING DATE: 1999-03-25
 NUMBER OF SEQ ID NOS: 10
 SOFTWARE: Patent In Ver. 2.0
 SEQ ID NO 10
 LENGTH: 451

TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-276-400-10

Query Match 50.6%; Score 1042.5; DB 2; Length 451;
 Best Local Similarity 72.2%; Pred. No. 2e-82; Indels 1; Gaps 1;
 Matches 197; Conservative 41; Mismatches 34;

QY 1 MAQWDPDQOEDTDSCTESVYKFDARSVTALLPPHPKNGPTLOERKSKYKATLITLYLIV 60
 DB 1 MEQWDFHNOQEDTDSCTESVYKFDARSMTALLPPHPKNSPSIQETLKSFKALLIALYLLV 60
 QY 61 FVVLVPIIGIYAAQLKMETKNCCTVGSVNA-DISSPBGKNGSGDEMRFRFAVVERNSN 119
 DB 61 FAVLIPILIGIYAAQLKMETKNCSSVSTNANDITQSLTGKNDSEEMRFOEFVMEHNSN 120
 QY 120 MESRIQYSDNEANLIDAKNFONFSITTDQRFNDVLPOLNSLSIOEHENIIGDISKL 179
 DB 121 MEKRIQHLIDNEANLMDTEHFONFSMTTDQRFNDILQLSTLFSVOGHNAIDISKL 180
 QY 180 VGLNTTVLDLQFSIETTLNGRVOENAFKQOEMRKLEERIYNASAEIKSLDEKQVYLEOEI 239
 DB 181 ISLNTTLLDLQNLINENLNGKIQENTFKQOEISKLEERYVNVSAIIMAKKEQVHLEOEI 240
 QY 240 KGEKMLNNITNDRLKDMESQTLKNTITLQ 272
 DB 241 KGEVAVLNNITNDRLKDMESQTLKNTITLQ 273

RESULT 13
 US-09-448-076-10
 Sequence 10, Application US/09448076
 Patent No. 6300092
 GENERAL INFORMATION:
 APPLICANT: Khodadoust, Mehran et al.
 TITLE OF INVENTION: METHODS OF USE OF A NOVEL LYSYL OXIDASE-RELATED PROTEIN
 FILE REFERENCE: WNI-073CP
 CURRENT APPLICATION NUMBER: US/09/448,076
 CURRENT FILING DATE: 1999-11-23
 EARLIER APPLICATION NUMBER: 60/117,580
 EARLIER FILING DATE: 1999-01-27
 EARLIER APPLICATION NUMBER: 09/276,400
 NUMBER OF SEQ ID NOS: 12
 SOFTWARE: Patent In Ver. 2.0
 SEQ ID NO 10
 LENGTH: 451
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-448-076-10

Query Match 50.6%; Score 1042.5; DB 2; Length 451;
 Best Local Similarity 72.2%; Pred. No. 2e-82; Indels 1; Gaps 1;
 Matches 197; Conservative 41; Mismatches 34;

QY 1 MAQWDPDQOEDTDSCTESVYKFDARSVTALLPPHPKNGPTLOERKSKYKATLITLYLIV 60
 DB 1 MEQWDFHNOQEDTDSCTESVYKFDARSMTALLPPHPKNSPSIQETLKSFKALLIALYLLV 60
 QY 61 FVVLVPIIGIYAAQLKMETKNCCTVGSVNA-DISSPBGKNGSGDEMRFRFAVVERNSN 119
 DB 61 FAVLIPILIGIYAAQLKMETKNCSSVSTNANDITQSLTGKNDSEEMRFOEFVMEHNSN 120
 QY 120 MESRIQYSDNEANLIDAKNFONFSITTDQRFNDVLPOLNSLSIOEHENIIGDISKL 179
 DB 121 MEKRIQHLIDNEANLMDTEHFONFSMTTDQRFNDILQLSTLFSVOGHNAIDISKL 180
 QY 180 VGLNTTVLDLQFSIETTLNGRVOENAFKQOEMRKLEERIYNASAEIKSLDEKQVYLEOEI 239
 DB 181 ISLNTTLLDLQNLINENLNGKIQENTFKQOEISKLEERYVNVSAIIMAKKEQVHLEOEI 240
 QY 240 KGEKMLNNITNDRLKDMESQTLKNTITLQ 272

Db 241 KGEVKVNNITNDLRLKQMEHSQTLRNITLLIG 273

RESULT 14

US-09-702-572-10
Sequence 10, Application US/09702572
Patent No. 6391602

GENERAL INFORMATION:

APPLICANT: Khodadoust, Mehran
TITLE OF INVENTION: NOVEL MSP-18 PROTEIN AND NUCLEIC ACID MOLECULES AND
TITLE OF INVENTION: USES THEREFOR
FILE REFERENCE: NMI-073
CURRENT APPLICATION NUMBER: US/09/702,572
CURRENT FILING DATE: 2000-10-31
PRIOR APPLICATION NUMBER: 09/276,400
PRIOR FILING DATE: 1999-03-25
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 10
LENGTH: 451
TYPE: PRT
ORGANISM: Homo sapiens
US-09-702-572-10

Query Match 50.6%; Score 1042.5; DB 2; Length 451;
Best Local Similarity 72.2%; Pred. No. 26-82;
Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;

QY 1 MAQWDPDQOEDTDCSTESVVFARSVTALLPPHPKNGPTLOERKSKYKALITLYLIV 60
DB 1 MEQWDFHNOQEDTDCSTESVVFARSMWALLPPHPKNSPSLOELKSKFKALIALYLLV 60
QY 61 FVVLVPIIGIYVAOQLKMETKCTVGSVNA-DISPSPEKNGSGSEDEMRFRRAVNERNSN 119
DB 61 FAVLIPILIGIYVAOQLKMETKCSVSTNANDITQSLTGKNGDSSEEMKFOEFMEHMSN 120
QY 120 MESRIQVLSDEANLIDAKNFQNSITTDQRFNDVLFQNLSSLSIOEHENIIGDISKL 179
DB 121 MEKRIQHLIDMEANLMDTEHFQNFMTTDQRFNDILQSLTFSSVQGHGNAIDISKL 180
QY 180 VGLNTTVLDLQPSIETLNGRVOENAFKQOENRKLBERIYNASAEIKSLDEKQVYLEOEI 239
DB 181 ISLNTTLLDLQNLINLNGKIQENFKQOEISKLEERYVNSAIIAMKEQVHLEOEI 240
QY 240 KGEVKVNNITNDLRLKQMEHSQTLRNITLLIG 272
DB 241 KGEVKVNNITNDLRLKQMEHSQTLRNITLLIG 273

RESULT 15

PCT-US96-08081-2
Sequence 2, Application PC/TUS9608081

GENERAL INFORMATION:

APPLICANT: SmithKline Beecham Corporation
TITLE OF INVENTION: Attachment Enhanced 293 Cells
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSES: SmithKline Beecham - Corporate Patents U.S.
STREET: Mailcode - UW2220, 709 Swedeland Road
CITY: King of Prussia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19406-5090
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/08081
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:

NAME: Jervis, Herbert H.
REGISTRATION NUMBER: 31,171
REFERENCE/DOCKET NUMBER: P50338
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 270-5019
TELEFAX: (610) 270-5090
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 451 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-08081-2

Query Match 50.6%; Score 1042.5; DB 4; Length 451;
Best Local Similarity 72.2%; Pred. No. 26-82;
Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;

QY 1 MAQWDPDQOEDTDCSTESVVFARSVTALLPPHPKNGPTLOERKSKYKALITLYLIV 60
DB 1 MEQWDFHNOQEDTDCSTESVVFARSMWALLPPHPKNSPSLOELKSKFKALIALYLLV 60
QY 61 FVVLVPIIGIYVAOQLKMETKCTVGSVNA-DISPSPEKNGSGSEDEMRFRRAVNERNSN 119
DB 61 FAVLIPILIGIYVAOQLKMETKCSVSTNANDITQSLTGKNGDSSEEMKFOEFMEHMSN 120
QY 120 MESRIQVLSDEANLIDAKNFQNSITTDQRFNDVLFQNLSSLSIOEHENIIGDISKL 179
DB 121 MEKRIQHLIDMEANLMDTEHFQNFMTTDQRFNDILQSLTFSSVQGHGNAIDISKL 180
QY 180 VGLNTTVLDLQPSIETLNGRVOENAFKQOENRKLBERIYNASAEIKSLDEKQVYLEOEI 239
DB 181 ISLNTTLLDLQNLINLNGKIQENFKQOEISKLEERYVNSAIIAMKEQVHLEOEI 240
QY 240 KGEVKVNNITNDLRLKQMEHSQTLRNITLLIG 272
DB 241 KGEVKVNNITNDLRLKQMEHSQTLRNITLLIG 273

Search completed: February 16, 2006, 17:06:39
Job time : 49 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 16, 2006, 17:06:02 / Search time 166 Seconds
(without alignments)
1006.818 Million cell updates/sec

Title: US-10-618-570-2

Perfect score: 2059
Sequence: 1 MAQMDPFDQOEDTDSCTES.....DKATRVGINIFTRLRTOKE 400

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBSCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBSCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2059	100.0	400	4	US-10-618-570-2
2	1042.5	50.6	358	4	US-10-326-186-6
3	1042.5	50.6	358	5	US-10-741-600-1394
4	1042.5	50.6	358	5	US-10-741-600-1397
5	1042.5	50.6	358	5	US-10-741-600-1398
6	1042.5	50.6	358	5	US-10-741-600-1396
7	1042.5	50.6	451	3	US-09-782-980-19
8	1042.5	50.6	451	3	US-09-909-743-10
9	1042.5	50.6	451	4	US-10-426-262-2
10	1042.5	50.6	451	4	US-10-423-543-80
11	1042.5	50.6	451	4	US-10-806-018-19
12	1042.5	50.6	451	5	US-10-741-600-1395
13	801	38.9	454	5	US-10-496-905-481
14	801	38.9	458	3	US-09-782-980-126
15	801	38.9	458	4	US-10-806-018-126
16	678	32.9	152	4	US-10-724-527-4
17	678	32.9	151	6	US-11-093-776-7
18	678	32.9	152	6	US-09-957-667-2
19	670	32.5	173	5	US-10-893-576-59
20	670	32.5	485	4	US-10-656-769-59
21	670	32.5	485	4	US-10-656-769-60
22	204	9.9	495	4	US-10-468-335-2
23	204	9.9	517	4	US-10-138-588-66
24	201	9.8	495	5	US-10-496-905-444
25	169	8.2	244	4	US-10-326-186-8
26	168.5	8.2	234	4	US-10-326-186-10
27	168.5	8.2	437	4	US-10-311-623-10

28	153	7.4	141	5	US-10-471-422-4	Sequence 4, App11
29	149.5	7.3	431	4	US-10-013-173-4	Sequence 4, App11
30	149.5	7.3	431	4	US-10-150-762-4	Sequence 4, App11
31	149.5	7.3	431	4	US-10-244-821-4	Sequence 4, App11
32	149	7.2	143	5	US-10-471-422-2	Sequence 2, App11
33	140	6.8	1064	4	US-10-173-461-5	Sequence 5, App11
34	138.5	6.7	160	4	US-10-460-524-8	Sequence 2, App11
35	138.5	6.7	183	4	US-10-013-173-2	Sequence 2, App11
36	138.5	6.7	183	4	US-10-150-762-2	Sequence 2, App11
37	138.5	6.7	183	4	US-10-244-821-2	Sequence 2, App11
38	138.5	6.7	183	6	US-11-093-776-11	Sequence 11, App1
39	138.5	6.7	412	4	US-10-013-173-6	Sequence 6, App11
40	138.5	6.7	412	4	US-10-150-762-6	Sequence 6, App11
41	138.5	6.7	412	4	US-10-244-821-6	Sequence 6, App11
42	138.5	6.7	421	3	US-09-938-270B-1	Sequence 1, App11
43	138.5	6.7	423	3	US/10/013	Sequence 8, App11
44	138.5	6.7	423	4	US/10/150	Sequence 8, App11
45	138.5	6.7	423	4	US/10/244	Sequence 8, App11

ALIGNMENTS

RESULT 1
US-10-618-570-2; Sequence 2, Application US/10618570
; Publication No. US20040185059A1Query Match 100.0%; Score 2059; DB 4; Length 400;
Beet Local Similarity 100.0%; Pred. No. 6.4e-161;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MAQMDPFDQOEDTDSCTESVFKDARSVTALPPHKNQPTLOEBKMSYKATLITLYIV	60
DB	1	MAQMDPFDQOEDTDSCTESVFKDARSVTALPPHKNQPTLOEBKMSYKATLITLYIV	60
QY	61	FVTLVPIIGIYAAQLKTKETKCTGVSNADISPEBEGKNGSEBDMRFRVYMERMSM	120
DB	61	FVTLVPIIGIYAAQLKTKETKCTGVSNADISPEBEGKNGSEBDMRFRVYMERMSM	120
QY	121	ESRIGYLSDBENKALDANKFONFSITTDORFNDVLPOLNSLSSIOEHNIIGDISKLV	180
DB	121	ESRIGYLSDBENKALDANKFONFSITTDORFNDVLPOLNSLSSIOEHNIIGDISKLV	180
QY	181	GLNTTVLDLQFSIETLNGRVQENAFKQOEBMKLEBRIYNSAKISLDEKQVYLEQETK	240
DB	181	GLNTTVLDLQFSIETLNGRVQENAFKQOEBMKLEBRIYNSAKISLDEKQVYLEQETK	240
QY	241	GEMKLIANNITVLDRLKQWEHSGTLNITLLQCARCSLTGKKTNDLGSMTTGAVNSRGE	300
DB	241	GEMKLIANNITVLDRLKQWEHSGTLNITLLQCARCSLTGKKTNDLGSMTTGAVNSRGE	300

QY	Db	QY	Db
301	301	361	361
FTCTYTAATAASNEKESPLGICONTINKRPPFGTAAWKKSESITVPGCFIDRN	FTCTYTAATAASNEKESPLGICONTINKRPPFGTAAWKKSESITVPGCFIDRN	GKEVLKTMILNLSVANDIGDDMKATRVGINITRLRTOKE	GKEVLKTMILNLSVANDIGDDMKATRVGINITRLRTOKE
301	301	361	361
FTCTYTAATAASNEKESPLGICONTINKRPPFGTAAWKKSESITVPGCFIDRN	FTCTYTAATAASNEKESPLGICONTINKRPPFGTAAWKKSESITVPGCFIDRN	GKEVLKTMILNLSVANDIGDDMKATRVGINITRLRTOKE	GKEVLKTMILNLSVANDIGDDMKATRVGINITRLRTOKE

RESULT 2

```

Sequence 6, Application US/10326186
Publication No. US20030119149A1
GENERAL INFORMATION:
APPLICANT: Reddy, Pranthitha
TITLE OF INVENTION: Tri-metric Recombinant Polypeptides
FILE REFERENCE: 3398-A
CURRENT APPLICATION NUMBER: US/10/326,186
CURRENT FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 358
TYPE: PRT
ORGANISM: Homo sapiens
US-10-326-186-6

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Query Match	50.6%	Score 1042.5;	DB 4;	Length 358;
Best Local Similarity	72.2%;	Pred. No. 3.1e-77;		
Matches 197;	Conservative 41;	Mismatches 34;	Indels 1;	Gaps 1;

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QY      1  MAOMDPEPDQOEBTDBCTSCSYKFDASVALLPBPBKNGPTLOEMKSYKALITLILV  60
Db      1  MEQMDHFHQOEBTDBCTSCSYKFDARSMYALLPBPBKNSPBLQETKMSFKAALLILV  60

QY      61  FVVLVPLIGIVAAQILKMETKQCTGVSUNA-DISPSPGKNGSEDEMRPREAVMEMSN  119
Db      61  FAVLIPILIGIVAAQILKMETKQCSVSTVANDITQSLGKNGDSSEEMRPFQEVMEHMSN  120

QY      120  MESRIQVLSNDNEANLLDAKQFONFSITTDQRPNDVLPONLISLSIOEHNIIDDISKL  179
Db      121  MEKRIOHILDMENANLLDTEHFONFSITTDQRPNDLILQSLSTFVSQCHGNAIDISKL  180

QY      180  VGLNTTVLIDQFSIETLNGRVOENAFKQOQEMKLEERIYNASAEISLDEKQVYLEOEI  239
Db      181  ISINTVLIDQNLINEMNGKIOENTFKQOEEISLEERVYVNSAIVAMKEEBOYHLEOEI  240

QY      240  KGEMLKLNNTTNDRLKDMESHQTLKNITLLOG  272
Db      241  KGEVYKLNNTTNDRLKDMESHQTLKNITLLOG  273

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RESULT 3

```

Sequence 1394, Application US/10741600
Publication No. US20050026169A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1394
LENGTH: 358
TYPE: PR1
ORGANISM: Homo sapiens
US-10-741-600-1394

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Query Match	50.6%;	Score 1042.5;	DB 5;	Length 358;
Best Local Similarity	72.2%;	Pred. No. 3.1e-77;		

Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;

Qy	1	MAOWNDPPDOOEPPDSCSESVKFDARSRVALLPBPBKGPPTLOBRKSKYKTLITLYLY	60
		1 MEOWNDPPDOOEPPDSCSESVKFDARSRVALLPBPBKGPPTLOBRKSKYKTLITLYLY	60
Db	1	MEOWNDPPDOOEPPDSCSESVKFDARSRVALLPBPBKGPPTLOBRKSKYKTLITLYLY	60
Qy	61	FVILVPIIGIYAAQLLKKMETKXONCTVGSVNA-DISEPBGKNGSEDEMRPREAWERMSN	119
		61 FVILVPIIGIYAAQLLKKMETKXONCTVGSVNA-DISEPBGKNGSEDEMRPREAWERMSN	119
Db	61	FVILVPIIGIYAAQLLKKMETKXONCTVGSVNA-DISEPBGKNGSEDEMRPREAWERMSN	120
Qy	120	MESHFOYSDNBEANLLDAKNFONPSITTDORPDVLPOLNSHLSSTIOEHNIIIGDISKSL	179
		120 MESHFOYSDNBEANLLDAKNFONPSITTDORPDVLPOLNSHLSSTIOEHNIIIGDISKSL	179
Db	121	MEKXIOHILDEANLMDTEHFONPESMTTIDQRNDNILLQJLSTLPSVQGHGNAIDELISKSL	180
Qy	180	VGLNTTVLIDLOFSEITTLGRVQENAFKQOEERKULBEERYNNAASAIKSLDEKOVYLEOEI	239
		180 VGLNTTVLIDLOFSEITTLGRVQENAFKQOEERKULBEERYNNAASAIKSLDEKOVYLEOEI	239
Db	181	ISLWTTLLDLOLNTENIENLNGKIOENTFKOOBEISKLBEERYNNAASAIKSLDEKOVYLEOEI	240
Qy	240	KGEMKLLNNTNDRLKDMESQTLAKNTITLLLOG	272
		240 KGEMKLLNNTNDRLKDMESQTLAKNTITLLLOG	272
Db	241	KGBYKVALNNTNDRLKDMESQTLAKNTITLLLOG	273

RESULT 4

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; Sequence 1397, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMERISMS
; TITLE OF INVENTION: MYOCARDIAL INFARCTIO
; FILE REFERENCE: CLO01499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: RastSeq for Windows Version 4.0
; SEQ ID NO 1397
; LENGTH: 358
; TYPE: PR1
; ORGANISM: Homo sapiens
US-10-741-600-1397

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Query Match	50.6%	Score 1042.5;	DB 5;	Length 358;
Best Local Similarity	72.2%;	Pred. No. 3,1e-77;		
Matches 197;	Conservative 41;	Mismatches 34;	Indels 1;	Gaps 1

```

QY 1 AAOWDDPDDPOEDPDSCTESVKYKPARSTYALPHPKPKNGPTYOEMKSKYKTAITYLYLY 60
Db 1 MEQMDHFNQOEDTSDSCESVAFEDKRSMTALPPHPKPSPSJOEKSKFRKALIALYLYV 60
QY 61 FVVLVPIIGIYAAQLKMKETKCTVGSVVA-DISBSPCKGKGSBEDEMFREAVERMSN 119
Db 61 FAVILPIGIVAAQLKMKETKCNCSYSINANITQSLTGKGNDSBEKMFQEVFMEHNS 120
QY 120 MESRQYISDNEMANILDAKFNQNSITTDQRPNDVLFOUNSLSSIOEHENIIGDISKSL 179
Db 121 MEKRIQHLIDMEANIMDTHEHFQNFSEMTTIDQRPNDILLOJSTLPSVOGGMALDESKSL 180
QY 180 VGLNTTVLIDLQFSLETLNGRVOENAFKQOEEMRKLEBRITYNASAEIKSLDEKQVYLEOET 239
Db 181 ISLNTLTDLQLNIFENLNGKIQENFPKQOEBISKLEBRYYNSAETIMAKKEOVHLEOET 240
QY 240 KGEKMLNNTNDALRKMEHSQTLKNTITLLOG 272
Db 241 KGEVAVLNNNTNDALKDMEHSQTLKNTITLLOG 273

```

RESULT 5

```

; Sequence 1398, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.

```

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1398
LENGTH: 358
TYPE: PRF
ORGANISM: Homo sapiens
US-10-741-600-1398

Query Match 50.6%; Score 1042.5; DB 5; Length 388;
Best Local Similarity 72.2%; Pred. No. 3.1e-77;
Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;

QY 1 MAOWDDPFDQOEDPTSCSYKFDARSVTALLPFPKNGPTLOERMSYKTALITLYIIV 60
DB 1 MEQMDHFNQOEDPTSCSYKFDARSMTALLPFPKNSPSLOERLKSFKALILYILV 60
QY 61 FVLVPIIGIYAAOQLKMETKCTGVSYNA-DISPSPEKNGSGSEDEMRPREAVMERMSN 119
DB 61 FVLVPIIGIYAAOQLKMETKCTGVSYNA-DISPSPEKNGSGSEDEMRPREAVMERMSN 120
QY 120 MESRIQYSDNEANILDAKFNQNSITTDQRFNDVLPQNLSSLSIOEHENIGDISKSL 179
DB 121 MEKIQHILDBEANILMDEHFQNFMTTDQRFNDVLPQNLSSLSIOEHENIGDISKSL 180
QY 180 VGLNTTVLDLQFSIETTLNGRVOENAFKQOEEMKLEERIYNASAEIKSLDEKQVYLEOEI 239
DB 181 ISLNTTLLDQLQNTIENLNGKIQENTFKQOEISKLEERVYVNASAIMAKKEQVHLEOEI 240
QY 240 KGEMLNNITNDLRLKQWESQTLRNITLLQG 272
DB 241 KGEVVLNNITNDLRLKQWESQTLRNITLLQG 273

RESULT 6
US-10-741-600-1396
Sequence 1396, Application US/10741600
Publication No. US20050026169A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1396
LENGTH: 388
TYPE: PRF
ORGANISM: Homo sapiens
US-10-741-600-1396

Query Match 50.6%; Score 1042.5; DB 5; Length 388;
Best Local Similarity 72.2%; Pred. No. 3.1e-77;
Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;

QY 1 MAOWDDPFDQOEDPTSCSYKFDARSVTALLPFPKNGPTLOERMSYKTALITLYIIV 60
DB 1 MEQMDHFNQOEDPTSCSYKFDARSMTALLPFPKNSPSLOERLKSFKALILYILV 60
QY 61 FVLVPIIGIYAAOQLKMETKCTGVSYNA-DISPSPEKNGSGSEDEMRPREAVMERMSN 119
DB 61 FVLVPIIGIYAAOQLKMETKCTGVSYNA-DISPSPEKNGSGSEDEMRPREAVMERMSN 120
QY 120 MESRIQYSDNEANILDAKFNQNSITTDQRFNDVLPQNLSSLSIOEHENIGDISKSL 179
DB 121 MEKIQHILDBEANILMDEHFQNFMTTDQRFNDVLPQNLSSLSIOEHENIGDISKSL 180

QY 180 VGLNTTVLDLQFSIETTLNGRVOENAFKQOEEMKLEERIYNASAEIKSLDEKQVYLEOEI 239
DB 181 ISLNTTLLDQLQNTIENLNGKIQENTFKQOEISKLEERVYVNASAIMAKKEQVHLEOEI 240
QY 240 KGEMLNNITNDLRLKQWESQTLRNITLLQG 272
DB 241 KGEVVLNNITNDLRLKQWESQTLRNITLLQG 273

RESULT 7
US-09-782-980-19
Sequence 19, Application US/09782980
Patent No. US20020072089A1
GENERAL INFORMATION:
APPLICANT: Rhododoust, Mehran M.
APPLICANT: Macbeth, Kyle J.
APPLICANT: Busfield, Samantha J.
APPLICANT: McCarthy, Sean A.
APPLICANT: Holtzman, Douglas A.
APPLICANT: Gu, Wei
APPLICANT: White, David

TITLE OF INVENTION: NOVEL ITALY, LOR-2, STRIFE, TRASH, BDSF, LRSG, AND
TITLE OF INVENTION: STMSR PROTEIN AND NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: MNI-121CP
CURRENT APPLICATION NUMBER: US/09/782,980
CURRENT FILING DATE: 2001-02-13
PRIOR APPLICATION NUMBER: PCT/US00/02125
PRIOR FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: 09/448,076
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: 09/276,400
PRIOR FILING DATE: 1999-03-25
PRIOR APPLICATION NUMBER: 60/117,580
PRIOR FILING DATE: 1999-01-27
PRIOR APPLICATION NUMBER: 09/014,195
PRIOR FILING DATE: 1998-01-27
PRIOR APPLICATION NUMBER: 09/014,348
PRIOR FILING DATE: 1998-01-27
PRIOR APPLICATION NUMBER: 09/086,892
PRIOR FILING DATE: 1998-05-29
PRIOR APPLICATION NUMBER: 09/296,208
PRIOR FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: 09/063,950
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 09/561,381
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 09/561,810
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 09/087,121
PRIOR FILING DATE: 1998-05-29
PRIOR APPLICATION NUMBER: 09/672,721
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 09/049,799
PRIOR FILING DATE: 1998-03-27
NUMBER OF SEQ ID NOS: 176
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 19
LENGTH: 451
TYPE: PRF
ORGANISM: Homo sapiens
US-09-782-980-19

Query Match 50.6%; Score 1042.5; DB 3; Length 451;
Best Local Similarity 72.2%; Pred. No. 4.3e-77;
Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;

QY 1 MAOWDDPFDQOEDPTSCSYKFDARSVTALLPFPKNGPTLOERMSYKTALITLYIIV 60
DB 1 MEQMDHFNQOEDPTSCSYKFDARSMTALLPFPKNSPSLOERLKSFKALILYILV 60
QY 61 FVLVPIIGIYAAOQLKMETKCTGVSYNA-DISPSPEKNGSGSEDEMRPREAVMERMSN 119

```

Db 61 FAVLIPILIGIAAQLMKETKNCVSSTNANDITQSLTGKNDSEEMRFOEVMEMHNSN 120
Qy 120 MESIQVLSNEANLDAKFNQFNSITTDQRFNDVLPLQNSLSIOEHENIIGDISKSL 179
Db 121 MEKIQHLDMEANLMDTEHFQNSMTTDQRFNDILQSLTFSSVQGHGAIDIEISKSL 180
Qy 180 VGLNTVYLDQFSIETLNGRVOENAFKQOEEMRKLEERINYASAEIKSLDEKQVYLEOEI 239
Db 181 ISLNTTLLDDQLNTEENLNGKIQENTFKQOEISKLEERVYVNSAEIYAMKEQVHLEOEI 240
Qy 240 KGEVKVNLNTNDRLKDMWHSQTLRNITLIG 272
Db 241 KGEVKVNLNTNDRLKDMWHSQTLRNITLIG 273

```

```

RESULT 8
US-09-909-743-10
Sequence 10, Application US/09909743
Patent No. US20020151007A1
GENERAL INFORMATION:
APPLICANT: Rhodadoust, Mehran et al.
TITLE OF INVENTION: METHODS OF USE OF A NOVEL LYSYL OXIDASE-RELATED
FILE REFERENCE: MNI-073CP
CURRENT FILING DATE: 2001-07-20
CURRENT APPLICATION NUMBER: US/09/909, 743
PRIOR FILING DATE: EARLIER FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/276,400
PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-25
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10
LENGTH: 451
TYPE: PRT
ORGANISM: Homo sapiens
US-09-909-743-10

```

```

Query Match 50.6%; Score 1042.5; DB 3; Length 451;
Best Local Similarity 72.2%; Pred. No. 4.3e-77;
Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;

Qy 1 MAQWDDPDDQEDTDSCTESVYKFDARSVTALLPFPKNGPTLOERMKSYKTALITLYLIY 60
Db 1 MEQWDHFNQOEDTDSCTESVYKFDARSVTALLPFPKNGPTLOERMKSYKTALITLYLIY 60
Qy 61 FVILVPIIGIYAAQLMKETKNCVSSTNANDITQSLTGKNDSEEMRFOEVMEMHNSN 119
Db 61 FAVLIPILIGIAAQLMKETKNCVSSTNANDITQSLTGKNDSEEMRFOEVMEMHNSN 120
Qy 120 MESIQVLSNEANLDAKFNQFNSITTDQRFNDVLPLQNSLSIOEHENIIGDISKSL 179
Db 121 MEKIQHLDMEANLMDTEHFQNSMTTDQRFNDILQSLTFSSVQGHGAIDIEISKSL 180
Qy 180 VGLNTVYLDQFSIETLNGRVOENAFKQOEEMRKLEERINYASAEIKSLDEKQVYLEOEI 239
Db 181 ISLNTTLLDDQLNTEENLNGKIQENTFKQOEISKLEERVYVNSAEIYAMKEQVHLEOEI 240
Qy 240 KGEVKVNLNTNDRLKDMWHSQTLRNITLIG 272
Db 241 KGEVKVNLNTNDRLKDMWHSQTLRNITLIG 273

```

```

RESULT 9
US-10-426-262-2
Sequence 2, Application US/10426262
Publication No. US20040018521A1
GENERAL INFORMATION:
APPLICANT: Xu, Jinfeng
APPLICANT: Meyers, Deborah
APPLICANT: Zheng, Sigun
APPLICANT: Walsh, Patrick C.

```

```

APPLICANT: Isaacs, William B.
APPLICANT: Bleecer, Eugene
TITLE OF INVENTION: MUTATIONS IN THE MACROPHAGE SCAVENGER RECEPTOR 1 GENE ALTER RISK
TITLE OF INVENTION: OF PROSTATE CANCER, ASTHMA, AND CARDIOVASCULAR DISEASE
FILE REFERENCE: 9151-23
CURRENT FILING DATE: 2003-05-01
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2
LENGTH: 451
TYPE: PRT
ORGANISM: Homo sapiens
US-10-426-262-2

```

```

Query Match 50.6%; Score 1042.5; DB 4; Length 451;
Best Local Similarity 72.2%; Pred. No. 4.3e-77;
Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;

Qy 1 MAQWDDPDDQEDTDSCTESVYKFDARSVTALLPFPKNGPTLOERMKSYKTALITLYLIY 60
Db 1 MEQWDHFNQOEDTDSCTESVYKFDARSVTALLPFPKNGPTLOERMKSYKTALITLYLIY 60
Qy 61 FVILVPIIGIYAAQLMKETKNCVSSTNANDITQSLTGKNDSEEMRFOEVMEMHNSN 119
Db 61 FAVLIPILIGIAAQLMKETKNCVSSTNANDITQSLTGKNDSEEMRFOEVMEMHNSN 120
Qy 120 MESIQVLSNEANLDAKFNQFNSITTDQRFNDVLPLQNSLSIOEHENIIGDISKSL 179
Db 121 MEKIQHLDMEANLMDTEHFQNSMTTDQRFNDILQSLTFSSVQGHGAIDIEISKSL 180
Qy 180 VGLNTVYLDQFSIETLNGRVOENAFKQOEEMRKLEERINYASAEIKSLDEKQVYLEOEI 239
Db 181 ISLNTTLLDDQLNTEENLNGKIQENTFKQOEISKLEERVYVNSAEIYAMKEQVHLEOEI 240
Qy 240 KGEVKVNLNTNDRLKDMWHSQTLRNITLIG 272
Db 241 KGEVKVNLNTNDRLKDMWHSQTLRNITLIG 273

```

```

RESULT 10
US-10-423-543-80
Sequence 80, Application US/10423543
Publication No. US20040058355A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Libermann, Rosana K.
APPLICANT: Hunter, John J.
APPLICANT: Meyers, Rachel E.
APPLICANT: Rudolph-Owen, Laura A.
APPLICANT: Curtiss, Rory A.J.
APPLICANT: Olandt, Peter J.
APPLICANT: Tsai, Fong-Ying
APPLICANT: Galvin, Katherine M.
APPLICANT: Chun, Miyoung
APPLICANT: Williamson, Mark J.
APPLICANT: Silos-Santiago, Immaculada
APPLICANT: Bandaru, Rajasekhar
TITLE OF INVENTION: NOVEL 21910, 56634, 55053, 2504, 15977,
TITLE OF INVENTION: 14760, 25501, 17903, 3700, 21539, 26176, 26343, 56638,
TITLE OF INVENTION: 18610, 33217, 21967, 11983, 11983, 38555 OR 593 MOLECULES
FILE REFERENCE: MP103-023ONMIM
CURRENT FILING DATE: 2003-04-25
CURRENT APPLICATION NUMBER: US/10/423, 543
PRIOR FILING DATE: 2003-04-25
PRIOR APPLICATION NUMBER: US 10/278, 036
PRIOR FILING DATE: 2002-10-22
PRIOR APPLICATION NUMBER: US 09/711, 216
PRIOR FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: US 60/205, 447
PRIOR FILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: US 10/012, 055
PRIOR FILING DATE: 2001-11-13

```



```

; PRIOR APPLICATION NUMBER: US 60/248,325
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 10/003,690
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/248,893
; PRIOR FILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: US 09/797,039
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 60/186,061
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: US 10/217,168
; PRIOR FILING DATE: 2002-08-12
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 80
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-423-543-80

```

```

Query Match      50.6%; Score 1042.5; DB 4; Length 451;
Best Local Similarity 72.2%; Pred. No. 4.3e-77;
Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;

```

```

QY 1 MAQWDDPDDQEDTDSCTESVYKFDARSVTALLPFPKNGPTLQERMSKYKTLITLYILV 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 MEQWDFHNOQEDTDSCTESVYKFDARSVTALLPFPKNGPTLQERMSKYKTLITLYILV 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 FVLVPIIGIIVAAQLKMKETKNCVGVNA-DISPSPEKGNGSEDEKRFREAVMERMSN 119
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 FVLVPIIGIIVAAQLKMKETKNCVGVNA-DISPSPEKGNGSEDEKRFREAVMERMSN 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 120 MESRIQYSDNEANLIDAKNFQNFSTITTDQRFNDVLPQLNSLSIQEHENIIGDISKL 179
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 121 MEKRIQHLIDMEANLMDTEHFQNFSTITTDQRFNDVLPQLNSLSIQEHENIIGDISKL 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 180 VGLNTTVLDQFSITLNGRVQENAFKQOEERKLEERYNARSIKSLDEKQVYLEOEI 239
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 181 ISLNTTLDLQNLINNGKIQENTFKQOEESKLEERYNARSISATIMAKESQVHLEOEI 240
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 240 KGEMLNNITNDLRLKDMESHQTLKNITLLQG 272
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 241 KGEVAVLNNITNDLRLKDMESHQTLKNITLLQG 273
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

```

RESULT 11
US-10-806-018-19
; Sequence 19, Application US/10806018
; Publication No. US20040176296A1
; GENERAL INFORMATION:
; APPLICANT: Knodadoust, Mehran M.
; APPLICANT: Macbeth, Kyle J.
; APPLICANT: Busfield, Samantha J.
; APPLICANT: McCarthy, Sean A.
; APPLICANT: Holzman, Douglas A.
; APPLICANT: Gu, Wei
; APPLICANT: White, David
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL ITALY, LOR-2, STRIFE, TRASH, BDSF, LRSG, AND
; TITLE OF INVENTION: STWST PROTEIN AND NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: MNT-121CP
; CURRENT APPLICATION NUMBER: US/10/806,018
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: US/09/782,980
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: PCT/US00/02125
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 09/448,076
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 09/276,400
; PRIOR FILING DATE: 1999-03-25

```

```

; PRIOR APPLICATION NUMBER: 60/117,580
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 09/014,195
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: 09/014,348
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: 09/086,892
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 09/296,208
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 09/063,950
; PRIOR FILING DATE: 1998-04-21
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 176
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-806-018-19

```

```

Query Match      50.6%; Score 1042.5; DB 4; Length 451;
Best Local Similarity 72.2%; Pred. No. 4.3e-77;
Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;

```

```

QY 1 MAQWDDPDDQEDTDSCTESVYKFDARSVTALLPFPKNGPTLQERMSKYKTLITLYILV 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 MEQWDFHNOQEDTDSCTESVYKFDARSVTALLPFPKNGPTLQERMSKYKTLITLYILV 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 FVLVPIIGIIVAAQLKMKETKNCVGVNA-DISPSPEKGNGSEDEKRFREAVMERMSN 119
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 FVLVPIIGIIVAAQLKMKETKNCVGVNA-DISPSPEKGNGSEDEKRFREAVMERMSN 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 120 MESRIQYSDNEANLIDAKNFQNFSTITTDQRFNDVLPQLNSLSIQEHENIIGDISKL 179
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 121 MEKRIQHLIDMEANLMDTEHFQNFSTITTDQRFNDVLPQLNSLSIQEHENIIGDISKL 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 180 VGLNTTVLDQFSITLNGRVQENAFKQOEERKLEERYNARSIKSLDEKQVYLEOEI 239
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 181 ISLNTTLDLQNLINNGKIQENTFKQOEESKLEERYNARSISATIMAKESQVHLEOEI 240
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 240 KGEMLNNITNDLRLKDMESHQTLKNITLLQG 272
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 241 KGEVAVLNNITNDLRLKDMESHQTLKNITLLQG 273
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

```

RESULT 12
US-10-741-600-1395
; Sequence 1395, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1395
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-741-600-1395

```

```

Query Match      50.6%; Score 1042.5; DB 5; Length 451;
Best Local Similarity 72.2%; Pred. No. 4.3e-77;
Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;

```

```

QY 1 MAQWDDPDDQEDTDSCTESVYKFDARSVTALLPFPKNGPTLQERMSKYKTLITLYILV 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 MEQWDFHNOQEDTDSCTESVYKFDARSVTALLPFPKNGPTLQERMSKYKTLITLYILV 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

QY 61 FVVLPIIGIYAQAOLKMKETKCTVGSVNA-DISPSPEKGNGSEDEMRFEAVMERKSN 119
 DB 61 FAVLIPILGIYAQAOLKMKETKCTVGSVNA-DISPSPEKGNGSEDEMRFEAVMERKSN 120
 QY 120 MESRIQVLSDEANILDKAFONFSITTDORFNDVLPOLNSLSISIOHEHNIIGDISKSL 179
 DB 121 MEKRIQHLIDEBANIMDEHMFONFSMTDORFNDVLPOLNSLSISIOHEHNIIGDISKSL 180
 QY 180 VGLNTVVDLQFSIETTLNGRVOENAFKQOEEMRKLEERIYNASAEIKSLDEKQVYLEQOI 239
 DB 181 ISLNTTLDLQNLINENLNGKIOENTFKQOEISKLEERVYVSAEIMAKKEQVHLEQOI 240
 QY 240 KGEMLLNNTNDLRLKDMESQTLKNITTLQ 272
 DB 241 KGEVVLNNTNDLRLKDMESQTLKNITTLQ 273

RESULT 13
 US-10-496-905-481
 / Sequence 481, Application US/10496905
 / Publication No. US20050192215A1
 / GENERAL INFORMATION:
 / APPLICANT: Ghosh, Malabika
 / APPLICANT: Tang, Y. Tom
 / APPLICANT: Wang, Jian-Rui
 / APPLICANT: Wang, Zhiwei
 / APPLICANT: Zhao, Qing
 / APPLICANT: Xu, Chongjun
 / APPLICANT: Mulero, Jullio J.
 / APPLICANT: Boyle, Bryan J.
 / TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL POLYPEPTIDES AND POLYNUC
 / FILE REFERENCE: HVS-BICIP/US
 / CURRENT FILING DATE: 2004-05-26
 / PRIOR APPLICATION NUMBER: US/10/496,905
 / PRIOR FILING DATE: 2000-01-21
 / PRIOR APPLICATION NUMBER: US 09/488,725
 / PRIOR FILING DATE: 2000-04-25
 / PRIOR APPLICATION NUMBER: PCT/US00/35017
 / PRIOR FILING DATE: 2000-12-22
 / PRIOR APPLICATION NUMBER: US 09/620,312
 / PRIOR FILING DATE: 2000-07-19
 / PRIOR APPLICATION NUMBER: PCT/US00/34263
 / PRIOR FILING DATE: 2000-12-26
 / PRIOR APPLICATION NUMBER: US 09/496,914
 / PRIOR FILING DATE: 2000-02-03
 / PRIOR APPLICATION NUMBER: US 09/560,875
 / PRIOR FILING DATE: 2000-04-27
 / PRIOR APPLICATION NUMBER: PCT/US01/03800
 / PRIOR FILING DATE: 2001-02-05
 / PRIOR APPLICATION NUMBER: US 09/598,075
 / PRIOR FILING DATE: 2000-06-20
 / PRIOR APPLICATION NUMBER: PCT/US01/04098
 / PRIOR FILING DATE: 2001-02-05
 / Remaining Prior Application data removed - See File Wrapper or PALM.
 / NUMBER OF SEQ ID NOS: 653
 / SOFTWARE: PatentIn version 3.1
 / SEQ ID NO 481
 / LENGTH: 454
 / TYPE: PRT
 / ORGANISM: Mus musculus
 US-10-496-905-481

Query Match 38.9%; Score 801; DB 5; Length 454;
 Best Local Similarity 59.4%; Pred. No. 3.4e-57;
 Matches 158; Conservative 46; Mismatches 60; Indels 2; Gaps 2;

QY 8 PDQOEDTSCSYKFDARSYATLPPHKNQPTLOEBKSYKATLTLYLVFVWLVPI 67
 DB 9 PHBRDADCSSESVFDRSMYASLPNHTKQSPVQEKSPKALILYLVFVWLVPI 68
 QY 68 IGIYAQAOLKMKETKCTVGSVNA-DISPSPEKGNGSEDEMRFEAVMERKSNMESRIQY 126

DB 69 VGIVTAQLMWMKNCIVCSHNTSDTSGPMKENTSNVEMRF-TIIMAHKMEERIQS 127
 QY 127 LSDNEANILDKAFONFSITTDORFNDVLPOLNSLSISIOHEHNIIGDISKSLVGLNTTV 186
 DB 128 ISNKAADIDGRQNSMTATDORLNDLQNLINENLNGKIOENTFKQOEISKLEERVYVSAEIMAKKEQVHLEQOI 187
 QY 187 LDLOFSIETTLNGRVOENAFKQOEEMRKLEERIYNASAEIKSLDEKQVYLEQOI 246
 DB 188 LDVQLHETTLHVRRESTATQOEDISKLEERVYVSAEIMAKKEQVHLEQOI 247
 QY 247 NNITNDLRLKDMESQTLKNITTLQ 272
 DB 248 NNITNDLRLKDMESQTLKNITTLQ 273

RESULT 14
 US-09-782-980-126
 / Sequence 126, Application US/09782980
 / Patent No. US20020072089A1
 / GENERAL INFORMATION:
 / APPLICANT: Khodadoust, Mehran M.
 / APPLICANT: MacBeth, Kyle J.
 / APPLICANT: Busfield, Samantha J.
 / APPLICANT: McCarthy, Sean A.
 / APPLICANT: Holtzman, Douglas A.
 / APPLICANT: Gu, Wei
 / APPLICANT: White, David
 / APPLICANT: Pan, Yang
 / TITLE OF INVENTION: NOVEL ITALY, IOR-2, STRIPE, TRASH, BDPF, LRSG, AND
 / TITLE OF INVENTION: STREET PROTEIN AND NUCLEIC ACID MOLECULES AND USES
 / FILE REFERENCE: MNI-121CP
 / CURRENT FILING DATE: 2001-02-13
 / PRIOR APPLICATION NUMBER: US/09/782,980
 / PRIOR FILING DATE: 2000-01-27
 / PRIOR APPLICATION NUMBER: 09/448,076
 / PRIOR FILING DATE: 1999-11-23
 / PRIOR APPLICATION NUMBER: 09/276,400
 / PRIOR FILING DATE: 1999-03-25
 / PRIOR APPLICATION NUMBER: 60/117,580
 / PRIOR FILING DATE: 1999-01-27
 / PRIOR APPLICATION NUMBER: 09/014,195
 / PRIOR FILING DATE: 1998-01-27
 / PRIOR APPLICATION NUMBER: 09/014,348
 / PRIOR FILING DATE: 1998-01-27
 / PRIOR APPLICATION NUMBER: 09/066,892
 / PRIOR FILING DATE: 1998-05-29
 / PRIOR APPLICATION NUMBER: 09/296,208
 / PRIOR FILING DATE: 1999-04-21
 / PRIOR APPLICATION NUMBER: 09/063,950
 / PRIOR FILING DATE: 1998-04-21
 / PRIOR APPLICATION NUMBER: 09/561,381
 / PRIOR FILING DATE: 2000-04-28
 / PRIOR APPLICATION NUMBER: 09/561,810
 / PRIOR FILING DATE: 2000-04-28
 / PRIOR APPLICATION NUMBER: 09/087,121
 / PRIOR FILING DATE: 1998-05-29
 / PRIOR APPLICATION NUMBER: 09/672,721
 / PRIOR FILING DATE: 2000-09-28
 / PRIOR APPLICATION NUMBER: 09/049,799
 / PRIOR FILING DATE: 1998-03-27
 / NUMBER OF SEQ ID NOS: 176
 / SOFTWARE: PatentIn Ver. 2.0
 / SEQ ID NO 126
 / LENGTH: 458
 / TYPE: PRT
 / ORGANISM: Mus Musculus
 US-09-782-980-126

Query Match 38.9%; Score 801; DB 3; Length 458;
 Best Local Similarity 59.4%; Pred. No. 3.5e-57;
 Matches 158; Conservative 46; Mismatches 60; Indels 2; Gaps 2;

Qy	8	PDOOEDTOSCTSYKFDASVTALPPHKNPGTYLOERMKSYTALITYLYIVFVVLPI	67
Db	13	PHERDADOCSSSYKFDASMTASLPHSTKNGSVQEKLSFCAIILALYLVAFALIPV	72
Qy	68	IGIYVAOLIKMETKNCCTGVSU-ADISPEBEGKNGSEDBMRFRVEMRMSNESTIQ	126
Db	73	VGIYVAOLIMMEMKCYLCYSRNTSDTOSQPEMEKNTSNVEMR-TIIMAMKMEERTIOS	131
Qy	127	LSDNEANLLDANFQNFSTTDOFRFNDVLFQNLSSLSIOEHNIIGDISKSLVGNITTV	186
Db	132	ISNSKQADLIDTGRFQNFSPATDORLANDILLQNLSSLSIOEHNSLDAISKLSQSLNMTL	191
Qy	187	LDOFSIFTLNGRVOENAFKQOEEMKLEERIYNASAEIKSLDEKOVYLEQOIKGENKL	246
Db	192	LDVOLHTEFLHRAVESTAKQOEDISKLEERVYKVAEVOSSVKEBOAHVEQOEKOEVRVL	251
Qy	247	NNITNDLRLKOMEHSGOTLKNIITFILOS	272
Db	252	NNIITNDLRLKOMEHSGOTLKNIITFILOS	277

RESULT 15
US-10-806-018-126
; Sequence 126, Application US/10806018
; Publication No. US20040176296A1
; Summary: INFORMATION

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1  GENERAL INFORMATION:
2  APPLICANT: Rhodadoust, Mehtran M.
3  APPLICANT: Macbeth, Kyle J.
4  APPLICANT: Busfield, Samantha J.
5  APPLICANT: McCarthy, Sean A.
6  APPLICANT: Holtzman, Douglas A.
7  APPLICANT: Gu, Wei
8  APPLICANT: White, David
9  TITLE OF INVENTION: NOVEL ITALY, LOR-2, STRIPE, TRASH, BDSF, IRSQ, AND
10 TITLE OF INVENTION: STMS* PROTEIN AND NUCLEIC ACID MOLECULES AND USES
11 FILE REFERENCE: THEREFOR
12 FILE REFERENCE: MMI-121CP
13 CURRENT APPLICATION NUMBER: US/10/806,018
14 PRIOR APPLICATION NUMBER: 2004-03-22
15 PRIOR FILING DATE: 2001-02-13
16 PRIOR APPLICATION NUMBER: PCT/US00/02125
17 PRIOR FILING DATE: 2000-01-27
18 PRIOR APPLICATION NUMBER: 09/448,076
19 PRIOR FILING DATE: 1999-11-23
20 PRIOR APPLICATION NUMBER: 09/276,400
21 PRIOR FILING DATE: 1999-03-25
22 PRIOR APPLICATION NUMBER: 60/117,580
23 PRIOR FILING DATE: 1999-01-27
24 PRIOR APPLICATION NUMBER: 09/014,195
25 PRIOR FILING DATE: 1998-01-27
26 PRIOR APPLICATION NUMBER: 09/014,348
27 PRIOR FILING DATE: 1998-01-27
28 PRIOR APPLICATION NUMBER: 09/086,892
29 PRIOR FILING DATE: 1998-05-29
30 PRIOR APPLICATION NUMBER: 09/296,208
31 PRIOR FILING DATE: 1999-04-21
32 PRIOR APPLICATION NUMBER: 09/063,950
33 PRIOR FILING DATE: 1998-04-21
34 Remaining Prior Application data removed - See File Wrapper or PALM.
35 NUMBER OF SEQ ID NOS: 176
36 SOFTWARE: PatentIn Ver. 2.0
37 SEQ ID NO 126
38 LENGTH: 458
39 TYPE: PRT
40 *ORGANISM: Mus Musculus
41 US-10-806-018-126

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Query Match	38.9%;	Score 801;	DB 4;	Length 458;
Best Local Similarity	59.4%;	Pred. No. 3.5e-57;		
Matches 158;	Conservative 46;	Mismatches 60;	Indels 2;	Gaps 2

[illegible]

Search completed: February 16, 2006, 17:09:31
Job time : 167 secs

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i

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November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases: older published applications make up the Published_Applications_Main databases.

- Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New).
- Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

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OM protein - protein search, using sw model

Run on: February 16, 2006, 17:06:52 ; Search time 18 Seconds

(without alignments)
315.881 Million cell updates/sec

Title: US-10-618-570-2

Perfect score: 2059
Sequence: 1 MAQWDDPPDOQEDPDSCTES.....DKMTRVGINIFTRLRTOKE 400

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 107819 seqs, 14214640 residues

Total number of hits satisfying chosen parameters: 107819

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:*

1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB pep: *
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB pep: *
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB pep: *
4: /cgn2_6/ptodata/1/pubpaa/PCOT_NEW_PUB pep: *
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6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB pep: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1042.5	50.6	358	US-10-995-561-885	Sequence 885, App
2	1042.5	50.6	358	US-10-995-561-888	Sequence 888, App
3	1042.5	50.6	358	US-10-995-561-889	Sequence 889, App
4	1042.5	50.6	388	US-10-995-561-889	Sequence 887, App
5	1042.5	50.6	451	US-10-995-561-886	Sequence 886, App
6	138.5	6.7	421	US-10-673-781-1	Sequence 1, Appli
7	135.5	6.6	270	US-11-123-696A-3	Sequence 169, App
8	129	6.3	1404	US-10-878-556A-159	Sequence 214, App
9	125.5	6.1	2665	US-11-124-368A-214	Sequence 215, App
10	125.5	6.1	2664	US-11-124-368A-215	Sequence 216, App
11	122.5	5.9	5024	US-10-793-626-2964	Sequence 1660, App
12	120	5.8	885	US-10-793-626-1660	Sequence 2, Appli
13	115.5	5.6	492	US-11-152-697-2	Sequence 5, Appli
14	115.5	5.6	539	US-11-152-697-5	Sequence 3154, App
15	110.5	5.4	1095	US-10-793-626-3154	Sequence 665, App
16	109.5	5.3	1266	US-10-995-561-665	Sequence 661, App
17	109.5	5.3	1652	US-10-995-561-661	Sequence 662, App
18	109.5	5.3	1938	US-10-995-561-662	Sequence 663, App
19	109.5	5.3	1934	US-10-995-561-660	Sequence 664, App
20	109.5	5.3	1954	US-10-995-561-660	Sequence 664, App
21	109.5	5.3	1972	US-10-995-561-666	Sequence 666, App
22	109.5	5.3	1972	US-10-995-561-666	Sequence 11, Appli
23	107.5	5.2	489	US-11-067-121-12	Sequence 12, Appli
24	106.5	5.2	496	US-11-129-076-7	Sequence 7, Appli
25	106.5	5.2	496	US-11-129-076-7	Sequence 7, Appli

26	106	5.1	373	US-11-072-512-1995	Sequence 1995, App
27	105.5	5.1	1562	US-11-052-554A-211	Sequence 211, App
28	105.5	5.1	1786	US-11-196-400-3	Sequence 3, Appli
29	104.5	5.1	1126	US-10-485-517-248	Sequence 248, App
30	104	5.1	955	US-11-052-554A-179	Sequence 179, App
31	104	5.1	1189	US-11-074-176-134	Sequence 134, App
32	102.5	5.0	706	US-10-485-517-146	Sequence 146, App
33	100.5	4.9	860	US-11-019-711-59	Sequence 59, Appli
34	100.5	4.9	862	US-11-128-420-11	Sequence 11, Appli
35	100.5	4.9	862	US-11-007-428-2	Sequence 2, Appli
36	100.5	4.9	862	US-11-183-294-16	Sequence 16, Appli
37	100	4.9	547	US-11-052-554A-285	Sequence 285, App
38	100	4.9	700	US-11-196-475-66	Sequence 66, Appli
39	99.5	4.8	335	US-10-453-372-426	Sequence 426, App
40	99.5	4.8	335	US-10-453-372-428	Sequence 428, App
41	99.5	4.8	446	US-11-098-686-10239	Sequence 10239, A
42	99.5	4.8	1538	US-10-995-561-772	Sequence 772, App
43	99.5	4.8	2107	US-10-995-561-827	Sequence 827, App
44	99.5	4.8	2480	US-10-995-561-825	Sequence 825, App
45	99.5	4.8	3116	US-10-995-561-826	Sequence 826, App

ALIGNMENTS

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RESULT 1
US-10-995-561-885
; Sequence 885, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 885
; LENGTH: 358
; TYPE: PRP
; ORGANISM: Homo sapiens
US-10-995-561-885

Query Match      50.6%; Score 1042.5; DB 6; Length 358;
Best Local Similarity 72.2%; Pred. No. 8.9e-67;
Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;

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   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 MEQWDFHQQEDPDSCTESVYKFDARSVTALPPHKKGPPTQOEKMSYKTLITLYLV 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 FVVLVPIIGIYAQAOLKWKETKCTVGSVNA-DISPSPEKNGSDEMRFREAVMERNSN 119
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 FAVLPIIGIYAQAOLKWKETKCTVGSVNA-DISPSPEKNGSDEMRFREAVMERNSN 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 120 MESRIQYISDNEANLIDAKNFONESITTDORNDVLPQANLSLSIOENHNTIGDISKL 179
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 121 MEKRIOHILIDMEANLIDAKNFONESITTDORNDVLPQANLSLSIOENHNTIGDISKL 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 180 VGLNTTVLDIOSIFETLNGVOENAFKQOEERKXLEERYNNAEATKSLDEQVYLEOEI 239
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 181 ISLNTTLLDLQNTLNKNGKIOENFQOEERKXLEERYNNAEATKSLDEQVYLEOEI 240
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 240 KGEVAVLNNITNDLRLKQWESQTLRNITLIG 272
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 241 KGEVAVLNNITNDLRLKQWESQTLRNITLIG 273
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 2
US-10-995-561-888
; Sequence 888, Application US/10995561

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Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: C1001559
CURRENT APPLICATION NUMBER: US/10/995,561
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 888
LENGTH: 358
TYPE: PRT
ORGANISM: Homo sapiens
US-10-995-561-888

Query Match      50.6%; Score 1042.5; DB 6; Length 358;
Best Local Similarity 72.2%; Pred. No. 8.9e-67;
Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;

OY 1 MAQWDPDQOEDPDSCTESVYKFDARSVTALLPBPKNKGPITLOERMSYKTALITLYIIV 60
DB 1 MEQWDHFNHQOEDPDSCTESVYKFDARSMTALLPBPKNKSPSLOEKLSFKKALLIALLYIV 60
OY 61 FVVLPIIGIYVAOQLLKMETKNCCTVGSVNA-DISPSPEKNGSGEDEMRFPEAVMERMSN 119
DB 61 FAVLIPILIGIYVAOQLLKMETKNCCTVGSVNA-DISPSPEKNGSGEDEMRFPEAVMERMSN 120
OY 120 MESRIQVLSDEANILDAKNFONFSITTDQRFNVLFPOLNSLSIOEHENIIGDISKL 179
DB 121 MEKRIQHLIDMEANILMDTEHFONFSMTTDQRFNDILQLSTLFSVQGHNAIDISKSL 180
OY 180 VGLNTTVLDLOFSIETLNGRVOENAFKQOEBMRKLEERIYNASAEIKSLDEKQVYLEOEI 239
DB 181 ISLNTTLLDLOLNTENLNKIQENTPFKQOEBISKLEERVYVSAEIMAKESQVHLEOEI 240
OY 240 KGEKMLNNITNDRLKDMESQTLKNTITLLOG 272
DB 241 KGEVYVANNITNDRLKDMESQTLKNTITLLOG 273

RESULT 3
US-10-995-561-889
Sequence 889, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: C1001559
CURRENT APPLICATION NUMBER: US/10/995,561
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 889
LENGTH: 358
TYPE: PRT
ORGANISM: Homo sapiens
US-10-995-561-889

Query Match      50.6%; Score 1042.5; DB 6; Length 358;
Best Local Similarity 72.2%; Pred. No. 8.9e-67;
Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;

OY 1 MAQWDPDQOEDPDSCTESVYKFDARSVTALLPBPKNKGPITLOERMSYKTALITLYIIV 60
DB 1 MEQWDHFNHQOEDPDSCTESVYKFDARSMTALLPBPKNKSPSLOEKLSFKKALLIALLYIV 60
OY 61 FVVLPIIGIYVAOQLLKMETKNCCTVGSVNA-DISPSPEKNGSGEDEMRFPEAVMERMSN 119
DB 61 FAVLIPILIGIYVAOQLLKMETKNCCTVGSVNA-DISPSPEKNGSGEDEMRFPEAVMERMSN 120
OY 120 MESRIQVLSDEANILDAKNFONFSITTDQRFNVLFPOLNSLSIOEHENIIGDISKL 179
DB 121 MEKRIQHLIDMEANILMDTEHFONFSMTTDQRFNDILQLSTLFSVQGHNAIDISKSL 180
OY 180 VGLNTTVLDLOFSIETLNGRVOENAFKQOEBMRKLEERIYNASAEIKSLDEKQVYLEOEI 239
DB 181 ISLNTTLLDLOLNTENLNKIQENTPFKQOEBISKLEERVYVSAEIMAKESQVHLEOEI 240
OY 240 KGEKMLNNITNDRLKDMESQTLKNTITLLOG 272
DB 241 KGEVYVANNITNDRLKDMESQTLKNTITLLOG 273

RESULT 4
US-10-995-561-887
Sequence 887, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: C1001559
CURRENT APPLICATION NUMBER: US/10/995,561
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 887
LENGTH: 388
TYPE: PRT
ORGANISM: Homo sapiens
US-10-995-561-887

Query Match      50.6%; Score 1042.5; DB 6; Length 388;
Best Local Similarity 72.2%; Pred. No. 9.9e-67;
Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;

OY 1 MAQWDPDQOEDPDSCTESVYKFDARSVTALLPBPKNKGPITLOERMSYKTALITLYIIV 60
DB 1 MEQWDHFNHQOEDPDSCTESVYKFDARSMTALLPBPKNKSPSLOEKLSFKKALLIALLYIV 60
OY 61 FVVLPIIGIYVAOQLLKMETKNCCTVGSVNA-DISPSPEKNGSGEDEMRFPEAVMERMSN 119
DB 61 FAVLIPILIGIYVAOQLLKMETKNCCTVGSVNA-DISPSPEKNGSGEDEMRFPEAVMERMSN 120
OY 120 MESRIQVLSDEANILDAKNFONFSITTDQRFNVLFPOLNSLSIOEHENIIGDISKL 179
DB 121 MEKRIQHLIDMEANILMDTEHFONFSMTTDQRFNDILQLSTLFSVQGHNAIDISKSL 180
OY 180 VGLNTTVLDLOFSIETLNGRVOENAFKQOEBMRKLEERIYNASAEIKSLDEKQVYLEOEI 239
DB 181 ISLNTTLLDLOLNTENLNKIQENTPFKQOEBISKLEERVYVSAEIMAKESQVHLEOEI 240
OY 240 KGEKMLNNITNDRLKDMESQTLKNTITLLOG 272
DB 241 KGEVYVANNITNDRLKDMESQTLKNTITLLOG 273

RESULT 5
US-10-995-561-886
Sequence 886, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: C1001559
CURRENT APPLICATION NUMBER: US/10/995,561
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSeq for Windows Version 4.0
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120 MESRIQVLSDEANILDAKNFONFSITTDQRFNVLFPOLNSLSIOEHENIIGDISKL 179
121 MEKRIQHLIDMEANILMDTEHFONFSMTTDQRFNDILQLSTLFSVQGHNAIDISKSL 180
OY 180 VGLNTTVLDLOFSIETLNGRVOENAFKQOEBMRKLEERIYNASAEIKSLDEKQVYLEOEI 239
DB 181 ISLNTTLLDLOLNTENLNKIQENTPFKQOEBISKLEERVYVSAEIMAKESQVHLEOEI 240
OY 240 KGEKMLNNITNDRLKDMESQTLKNTITLLOG 272
DB 241 KGEVYVANNITNDRLKDMESQTLKNTITLLOG 273

RESULT 4
US-10-995-561-887
Sequence 887, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: C1001559
CURRENT APPLICATION NUMBER: US/10/995,561
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 887
LENGTH: 388
TYPE: PRT
ORGANISM: Homo sapiens
US-10-995-561-887

Query Match      50.6%; Score 1042.5; DB 6; Length 388;
Best Local Similarity 72.2%; Pred. No. 9.9e-67;
Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;

OY 1 MAQWDPDQOEDPDSCTESVYKFDARSVTALLPBPKNKGPITLOERMSYKTALITLYIIV 60
DB 1 MEQWDHFNHQOEDPDSCTESVYKFDARSMTALLPBPKNKSPSLOEKLSFKKALLIALLYIV 60
OY 61 FVVLPIIGIYVAOQLLKMETKNCCTVGSVNA-DISPSPEKNGSGEDEMRFPEAVMERMSN 119
DB 61 FAVLIPILIGIYVAOQLLKMETKNCCTVGSVNA-DISPSPEKNGSGEDEMRFPEAVMERMSN 120
OY 120 MESRIQVLSDEANILDAKNFONFSITTDQRFNVLFPOLNSLSIOEHENIIGDISKL 179
DB 121 MEKRIQHLIDMEANILMDTEHFONFSMTTDQRFNDILQLSTLFSVQGHNAIDISKSL 180
OY 180 VGLNTTVLDLOFSIETLNGRVOENAFKQOEBMRKLEERIYNASAEIKSLDEKQVYLEOEI 239
DB 181 ISLNTTLLDLOLNTENLNKIQENTPFKQOEBISKLEERVYVSAEIMAKESQVHLEOEI 240
OY 240 KGEKMLNNITNDRLKDMESQTLKNTITLLOG 272
DB 241 KGEVYVANNITNDRLKDMESQTLKNTITLLOG 273

RESULT 5
US-10-995-561-886
Sequence 886, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: C1001559
CURRENT APPLICATION NUMBER: US/10/995,561
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSeq for Windows Version 4.0
```


SEQ ID NO 886
LENGTH: 451
TYPE: PRT
ORGANISM: Homo sapiens
US-10-995-561-886

Query Match 50.6%; Score 1042.5; DB 6; Length 451;
Best Local Similarity 72.2%; Pred. No. 1.2e-66;
Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;

QY 1 MAQWDPDQOEDTSCIESVFKDARSVTALLPPHPKNGPTLOEEMKSYKALITLYLYIV 60
DB 1 MEQWHPHQOEDTSCIESVFKDARSVTALLPPHPKNSPSIQEKLKSPKALILYLYIV 60
QY 61 FVNVPIIGIYVAOLKXETKCTGVSVA--DISSPKSGKSGDEMFRAVWERN 119
DB 61 FAVLPLGIYVAOLKXETKCTGVSVA--DISSPKSGKSGDEMFRAVWERN 120
QY 120 MESRIQYSDNEANLLDAKFNPSITTDQRENDVLFQNLSSIOEHENIIGDISKL 179
DB 121 MEKROHLDKMANLMDTEHFNFSMTTDQRENDILQSTLFSVQGGNAILDEISKL 180
QY 180 VGLNTTVLDLOFSITLNGRVOENAFKQOEKRLBERLYNASAEIKSLDEKQVLYDEI 239
DB 181 ISLNTTLLDLQNLINENLNGKIQENTFKQOEISKLDERVYVSAEIMAKKEQVHLQEI 240
QY 240 KGEMLNNITNDLRLKXWESQTLKNITLLQG 272
DB 241 KGEVKNNTNDLRLKXWESQTLKNITLLQG 273

RESULT 6
US-10-673-781-1
Sequence 1, Application US/10673781
Publication No. US20050260689A1

GENERAL INFORMATION:
APPLICANT: Olmwei Shi
TITLE OF INVENTION: Differential Immunoassay
FILE REFERENCE: 1112-1-080N
CURRENT APPLICATION NUMBER: US/10/673,781
CURRENT FILING DATE: 2003-09-29
PRIOR APPLICATION NUMBER: US/09/938,270B
PRIOR FILING DATE: 2001-08-23
PRIOR APPLICATION NUMBER: US 60/227,536
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/292,497
PRIOR FILING DATE: 2001-05-21
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PaetSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 421
TYPE: PRT
ORGANISM: homoeaplen
US-10-673-781-1

Query Match 6.7%; Score 138.5; DB 6; Length 421;
Best Local Similarity 33.1%; Pred. No. 0.0091;
Matches 43; Conservative 18; Mismatches 56; Indels 13; Gaps 7;

QY 273 ARKSLTGKWTNDGSMNTIGAVNSRGEFTGYITAV-TATSNIKESPLHGTONINKRQ 331
DB 13 AAAGITGWTNQDSTFIYVA-GADGALTGYBSAVGASRYVLTGRYDSAPATDQSG 71
QY 332 TOPFTGFTYVWK---FSESTVFTGQCFIDRNGKEV-LKTMWLLRSSVNDIGDMDKATR 386
DB 72 T--ALGWTYVAMKNNRYNAHSATWTSQYV---GGAEARINTQWLLTSGTTE-ANAMKSTYL 125
QY 387 VGINIFTRLR 396
DB 126 VGHDTFTKVK 135

RESULT 7

US-11-123-696A-3
Sequence 3, Application US/11123696A
Publication No. US20060024766A1
GENERAL INFORMATION:

APPLICANT: ATWELL, JOHN LESLIE
APPLICANT: DEVINE, PETER LEONARD
APPLICANT: KORTY, ALEXANDER ANDREW
APPLICANT: PERRY, GILLIAN WENDY
APPLICANT: BUNDESEN, PETER GREGORY
TITLE OF INVENTION: FUNCTIONAL MOLECULES
FILE REFERENCE: 674537-2001.1
CURRENT APPLICATION NUMBER: US/11/123,696A
CURRENT FILING DATE: 2005-05-05
PRIOR APPLICATION NUMBER: 09/581,924
PRIOR FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: PCT/AU98/01076
PRIOR FILING DATE: 1998-12-24
PRIOR APPLICATION NUMBER: AU PP1110
PRIOR FILING DATE: 1997-12-24
PRIOR APPLICATION NUMBER: AU PP5176
PRIOR FILING DATE: 1998-08-11
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patencin Ver. 3.3
SEQ ID NO 3
LENGTH: 270
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: construct of S. avidin and human immunoglobulin
US-11-123-696A-3

Query Match 6.6%; Score 135.5; DB 7; Length 270;
Best Local Similarity 32.8%; Pred. No. 0.0082;
Matches 42; Conservative 18; Mismatches 55; Indels 13; Gaps 7;

QY 275 KCSLTKGKWTNDGSMNTIGAVNSRGEFTGYITAV-TATSNIKESPLHGTONINKRQ 333
DB 23 EAGITGWTNQDSTFIYVA-GADGALTGYBSAVGASRYVLTGRYDSAPATDQSG- 80
QY 334 PFTGFTYVWK---FSESTVFTGQCFIDRNGKEV-LKTMWLLRSSVNDIGDMDKATR 388
DB 81 -ALGWTYVAMKNNRYNAHSATWTSQYV---GGAEARINTQWLLTSGTTE-ANAMKSTYL 135
QY 388 INIFTRLR 396
DB 136 HDTFTKVK 143

RESULT 8
US-10-878-556A-169
Sequence 169, Application US/10878556A
Publication No. US20050266399A1

GENERAL INFORMATION:
APPLICANT: Hoffmann La-Roche Inc.
TITLE OF INVENTION: HCV regulated protein expression
FILE REFERENCE: 21762
CURRENT APPLICATION NUMBER: US/10/878,556A
CURRENT FILING DATE: 2004-06-28
NUMBER OF SEQ ID NOS: 199
SOFTWARE: Patencin version 3.1
SEQ ID NO 169
LENGTH: 1404
TYPE: PRT
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: humangp/chr12-q14221
DATABASE ENTRY DATE: 2003-04-22
US-10-878-556A-169

Query Match 6.3%; Score 129; DB 6; Length 1404;
Best Local Similarity 21.5%; Pred. No. 0.21;
Matches 98; Conservative 69; Mismatches 175; Indels 114; Gaps 18;


```

Db      1164 KNEELKNEELTLEHETER-----LELAQKLNENVEEKSITTERKYLKELQSFETERHHL 1219
Qy      298 RGEFTGYITAVTATSNIEKES-----PLHGTONINKRTOPTGFTV----- 340
Db      1220 RG-----YIREIATGLOTKELKIAHILKHEQETIDELRVSSEKTAQIINTODLEKS 1274
Qy      341 NKPSESTVPTGOCFIDNGKEVAKTMMILRSSVNDI 378
Db      1275 HTKLOEETPLVHEOEELPNVENSET-----OETMNEL 1308

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RESULT 11

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US-10-793-626-2964
; Sequence 2964, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PUS480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; PRIOR FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2964
; LENGTH: 5024
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
; NAME/KEY: MOD RES
; LOCATION: (5024)
; OTHER INFORMATION: variable amino acid
US-10-793-626-2964

```

Query Match 5.9%; Score 122.5; DB 6; Length 5024;

Best Local Similarity 21.5%; Pred. No. 3.3;

Matches 90; Conservative 64; Mismatches 153; Indels 111; Gaps 17;

```

Qy      73 AQLKMKETKNCVGSVNDISPPSGKNGSEDEMRFRFAV-----MERMSNMESRIQYL 127
Db      324 AKLTK--AKEDAVASIN-NLS-----GLTNEQKTKENQAVNGSOTRQDVAVVLRDSKAL 374
Qy      128 SDNEANLLDAKNFQNFSTTDDQRFNDVL.FQLNSLSSIOEHENII-----GDISKSLVG- 181
Db      375 DOSMOTLADLVNNOVHISTSYNFPEDSTQKTYDNALDNGSTYITGCHNSLANSSTIDQ 434
Qy      182 ----LNTTVLDI-----QFSIE--TLNG-----RVQ-- 202
Db      435 TISQINTANGLHGAELQORDKGTANOEIGQLGYLANDPQKSAEELVNGSNTRSEVEEHL 494
Qy      203 -----NAFKQSEMRKLEERIVYASAEIKSLDEKQVYLBEGTIGEMKLNITNDRL 255
Db      495 NEAKSLNNAKQKLRDKVAEKTVNKOSSDYINDSTHORGVDQALQEAENIINIEINP--TL 553
Qy      256 KDMESQTLKNIT-----LLOGAKKCSLT-----GKMTNDLGSNMTI 292
Db      554 NKSEIEQKLOUTDQNALQSGHLEBAKNNAITEINKLTALNDARQRAIENVAQOTTI 613
Qy      293 GAVNSRGEFTGYITAVTATSNIEI-KESPLHGTONINKRTOPTGFTVNMKFSSESTVTF 351
Db      614 PAVNQOULTDREINFMQLRDVKVGOQNNVHOOSNYFNEDEQP-----KHNYDNSVQ 665
Qy      352 TGQCCIDR-----NGKEV-----LKTMMILRSSVNDIGDWMKATRVGINIFTLRT 397
Db      666 AGCTIIDKLODPIMKNKEIEQAINQIINTOTALSGENKLTHTQDSSTNRQIEGLSLSLNT 723

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RESULT 12

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US-10-793-626-1660
; Sequence 1660, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PUS480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; PRIOR FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1660
; LENGTH: 885
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-1660

```

Query Match 5.8%; Score 120; DB 6; Length 885;

Best Local Similarity 23.4%; Pred. No. 0.49;

Matches 45; Conservative 41; Mismatches 72; Indels 34; Gaps 7;

```

Qy      97 BEKGNGSEDEMRFRFAVNMERSNMESRIQYL-----SDNEANLLDAKNFQNFSTTDDQFN 152
Db      108 ERKKQSEETNARYE-----BEDNLNESQIDSIKNERAKOEKLAELKKNQ-----KQLN 156
Qy      153 DVL.FQLNSL-L-SSIOEHENIIIGDISKSLVGLNTTVLDI.QFSIETLNGRVOEN----- 203
Db      157 KEVOLESLIYSDQHQBKEIKNSYVTLMSBGSDVANNDRFLFHTINENBAKSRD 216
Qy      204 ----APKQ-----QEMRKLEERIVYASAEIKSLDEKQVYLBEGTIGEMKLNITNDIR 254
Db      217 SRLVAFNQLKDIOQNIQTQTOKEQYSSKSMKEVKNIQOLEQULTDSKRLSEYENKL- 275
Qy      255 LKDMESQTLKN 266
Db      276 YQAYRNEKLS 287

```

RESULT 13

```

US-11-152-697-2
; Sequence 2, Application US/11152697
; Publication No. US20060003367A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL HUMAN KUPFER CELL RECEPTOR
; FILE REFERENCE: D0242 NP
; CURRENT APPLICATION NUMBER: US/11/152,697
; PRIOR FILING DATE: 2005-06-14
; PRIOR APPLICATION NUMBER: 60/580,006
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 492
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-152-697-2

```

Query Match 5.6%; Score 115.5; DB 7; Length 492;

Best Local Similarity 20.9%; Pred. No. 0.47;

Matches 77; Conservative 53; Mismatches 136; Indels 103; Gaps 14;

```

Qy      70 IYAALDKETKNCVGSVNDISPPSGKNGSEDEMRFRFAVNMERSNMESRIQYLSLD 129
Db      57 VVEIOMLK-----CRVDVNSQLQVLDGHLGNTNAD-IQWVGKVLKDATTLSLQOTMLRS 110
Qy      130 NEANLLDAKNFQNFSTTDDQRFNDVL-FQ-LNSLSSIOEHENIIIGDISKSLVGLNTTVL 187

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      111 S-----LEGNAEIQLEKEDLEKADALFTQTLNFKSLSENTSIEHLVLSRGLNANSIEIQ 166
      188 DLQSIETLNGRVQ-----ENAFKQ-----QEEARK 213
      167 MLNMLETANTQALANSSLKNAAEIYVLRGHLDSVNDLRTONQVNLNLSGANAEIQG 226
      214 LEEERY-----NASAEIKSL-----DEKQVYLE--- 236
      227 LKENQNTNALSQTOAFIKSPDNTSAEIQFLRGLERAGDEIHVLRDLKMYAQTOK 286
      237 -----QEIKEKMLNNTNDLRKDMWHSQTLKNI-TLLOGARKCSLTGKMT 283
      287 ANGRLDQDTQIQVFKESEMNVTNLNAQIQVNLGHMKNASREIQTLKQGMKNASALTSQT 346
      284 NDIGSNMTIGAV---NSRGEFTGYITAVTATSNIKESPLHG--TQNTINKRTOPTFGF 338
      347 QMLDSNLQKASAEIQRLRGDLNLTALTWETIQEESRLKTLHVITTSQEQOLQRTQSOLIQ 406
      339 TV--NMKFS 345
      407 MVLOGMKFN 415

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RESULT 14
US-11-152-697-5
; Sequence 5, Application US/11152697
; Publication No. US20060003367A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL HUMAN KUPFER CELL RECEPTOR
; FILE REFERENCE: D0242 NP
; CURRENT APPLICATION NUMBER: US/11/152,697
; CURRENT FILING DATE: 2005-06-14
; PRIOR APPLICATION NUMBER: 60/580,006
; PRIOR FILING DATE: 2004-06-15
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 539
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-152-697-5

```

```

Query Match      5.6%; Score 115.5; DB 7; Length 539;
Best Local Similarity 20.9%; Pred. No. 0.53;
Matches 77; Conservative 53; Mismatches 136; Indels 103; Gaps 14;

```

```

      70 IVAQLKMETKCTVGSVNADISPSFGKNGSEDEMRFEAVVMESNMESRIQYLSQ 129
      118 VVEIQMLK-----CRVDVNSQLQVLGDLHGTNTND-IQWVGVLKADATTLISLOQLMRS 171
      130 NEANLLDANKFONFSITTDQRFNDVL-FQ-INSLLSSIQEHENITIGDISKSLVGLNTTVL 187
      172 S-----LEGNTNAEIQRLKEKDEKADALFTQTLNFKSLSENTSIEHLVLSRGLNANSIEIQ 227
      188 DLQSIETLNGRVQ-----ENAFKQ-----QEEARK 213
      228 MLNMLETANTQALANSSLKNAAEIYVLRGHLDSVNDLRTONQVNLNLSGANAEIQG 287
      214 LEEERY-----NASAEIKSL-----DEKQVYLE--- 236
      288 LKENQNTNALSQTOAFIKSPDNTSAEIQFLRGLERAGDEIHVLRDLKMYAQTOK 347
      237 -----QEIKEKMLNNTNDLRKDMWHSQTLKNI-TLLOGARKCSLTGKMT 283
      348 ANGRLDQDTQIQVFKESEMNVTNLNAQIQVNLGHMKNASREIQTLKQGMKNASALTSQT 407
      284 NDIGSNMTIGAV---NSRGEFTGYITAVTATSNIKESPLHG--TQNTINKRTOPTFGF 338
      408 QMLDSNLQKASAEIQRLRGDLNLTALTWETIQEESRLKTLHVITTSQEQOLQRTQSOLIQ 467

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QY      339 TV--NMKFS 345
DB      468 MVLOGMKFN 476

```

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RESULT 15
US-10-793-626-3154
; Sequence 3154, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMBERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: P03480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3154
; LENGTH: 1095
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-793-626-3154

```

```

Query Match      5.4%; Score 110.5; DB 6; Length 1095;
Best Local Similarity 20.8%; Pred. No. 3.1;
Matches 71; Conservative 59; Mismatches 125; Indels 87; Gaps 14;

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      111 EAVVMESNMESRIQYLSQNEANLLDANKFONFSIT-----TDQRFNDVLFOQLNSQL 162
      469 EAVQLKVNDAIHTMLQNKENNSA-LVTAKNQLQAVNPDPLTGTGTQDSINNVAKRNEAQ 527
      163 SSIOEHENIT--GD-----ISKSLVGLN-----TVVLDIQSIETLNGRVQ 201
      528 SAIRNAEAVINNGDATALAKQISDEKSKYQALAHNDAKQQLTADTTEIQTAVQQLNRBGD 587
      202 ENAFKQ-----EEMKLERIYNASAEISLDEKQVYLEQEIKEKMLNNTNDL-- 253
      588 TNNKKPRINAYNKAISLQSLQTSAKDANANAVIQPIRTVQEVNNALQVNLNQQLTE 647
      254 ---RLKDMWHSQTLK-----NITLLOGARKCSLTGKMTNDIGS 288
      648 AINQLOPLSNNDALKARLNLENKINQVOTDGMTQOSIEAVQNAKRYA-----QNE--S 700
      701 NTALALINN-GDADEQQLTTEITDRVN-----QOTTN-LTQALINGLTVNKEPLE-- 746
      349 TVFTGCCFIDBNGKEVLKTMVLLRSSVNDIGDDMKATRVGIN 390
      747 ---TAKTALQNNIDQVPSDGMTQOSVANYNQKLQIAKNEIN 785

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Search completed: February 16, 2006, 17:09:55
Job time : 20 secs

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